Title: Perfect score:

Sequence:

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Scoring table:

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APPLICANT: Braford Goldberg, Sarah R.
APPLICANT: Caparon, Maire H.
APPLICANT: Caparon, Maire H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Paik, Kumnan
APPLICANT: Paik, Kumnan
APPLICANT: Poik, Kumnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Co-administration of Interleukin-3
TITLE OF INVENTION: Mutant Polypeptides with CSF's for Multi-lineage
TITLE OF INVENTION: Hematopoletic Cell Production
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                            Sedineuroe 
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/471,045
FILING DATE: 06-JUN-1995
                      US-08-469-318-60
US-08-469-318-87
US-08-468-609A-60
US-08-468-609A-87
PCT-US95-01185-60
PCT-US95-01185-87
US-08-469-318-84
US-08-469-318-67
US-08-469-318-67
US-08-469-318-67
US-08-469-318-56
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PRICATION NUMBER: PCT/US95/01184
PRICATION NUMBER: PCT/US95/01184
FILING DATE: 02-FEB-1995
PRICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/193,373
FILING DATE: 04-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REGISTRATION NUMBER: 34,547
TELECOMUNICATION INFORMATION:
TELECHONE: (708)470-6801
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 57, Application US/08471045 Patent No. 6060047 GENERAL INFORMATION:
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Braford-Goldberg,
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Sequence 3, Appli
Sequence 18, Appl
Sequence 11, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 18, Appli
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Sequence 57, Appl
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1 ATGGAGCTGACTGAATTGCT.....TACGCCACCTTGCCCAGCCC 1095
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-347-029-3
US-08-457-254-3
US-08-484-257-18
US-08-999-212-1
US-08-999-97-1
PCT-US94-08806-18
PCT-US95-14932-3
PCT-US95-14626-3
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US-08-591-070A-1
US-08-413-803-24
US-08-321-488A-24
US-08-414-161B-1
US-08-927-855-1
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PCT-US95-03776-26
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US-08-388-779A-3
US-08-591-070A-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          - nucleic search, using sw model
                                                                                                                                                                                                      April 5, 2002, 10:34:58
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Gapop 10.0 , Gapext 1.0
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                            COUNTRY:
ZIP: 606
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                                                                                                                       Length 1059;
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Mutant Polypeptides with CSF's for
Hematopoietic Cell Production
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STREET: P. O. Box 5110
                                                                                                                    Score 518.8; DB 3;
Pred. No. 1.4e-116;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 57, Application US/08469712A
Patent No. 609395
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Caparon, Maire H.
APPLICANT: Caparon, Maire H.
APPLICANT: Eston, Alan M.
APPLICANT: Paston, Alan M.
APPLICANT: Patenn, John P.
APPLICANT: Olins, Peter O.
APPLICANT: Paik, Kumnan
APPLICANT: Paik, Kumnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Metant Polypeptign TITLE OF INVENTION: Hematopoietic Ce, NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
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 LENGTH: 1059 base pairs
; TYPE: nucleic acid
; STRANDEDRES: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-471-045-57
                                                                                                                       47.4%;
99.6%;
                                                                                                                    Query Match 47.4
Best Local Similarity 99.6
Matches 520; Conservative
SEQUENCE CHARACTERISTICS LENGTH: 1059 base pair
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US-08-469-712A-57
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                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPLIANTON NUMBER: US/08/469,712A
FILING DATE: 06.JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 47.4%; Score 518.8; DB 3; Best Local Similarity 99.6%; Pred. No. 1.4e-116; Matches 520; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01184
FILING DATE: 02-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/193,373
FILING DATE: 04-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2789/2
RELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1059 base pairs
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EDNESS: double
COMPUTER READABLE FORM:
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421 GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAGGTG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PURIFIED THROMBOPOIETIN AND METHOD MAKING IT
                                                                                                                                                                                                                                                                                     481 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOUTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/457,254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 518.8; DB 2;
Pred. No. 1.4e-116;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                          481 CGTTCCTGATGCTTGTAGGAGGGTCCACCTCTGCGTCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: FOISTCOM, John W
APPLICANT: Lofton-Day, Catherine E
APPLICANT: Lok, Si,
TITLE OF INVENTION: PURIFIED THROMBOP
TITLE OF INVENTION: MAKING IT
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 94-11
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6673
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08457254 Patent No. 5986049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.4%;
ilarity 99.6%;
Conservative
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
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Best Local Similarity
Matches 520; Conserv
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                     US-08-457-254-3
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                                                                                                                                                                            APPLICANT: Foster, Donald C.
APPLICANT: Helpel, Mark
APPLICANT: Holly, Richard D.
TITLE OF INVENTION: METHOD FOR SECRETING THROMBOPOLETIN
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,029
                                                                                                                                                                                                                                                                                                                         ADDRESSEE: 2ymoGenetics, Inc. STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: PATKET, GAYP
REGISTRATION NUMBER: 31-648
REFERENCE//DOCKET NUMBER: 94-12
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6673
                                                                                                                     Sequence 3, Application US/08347029
Patent No. 5641655
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                          98102
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US-08-347-029-3
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                US-08-347-029-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Fibbe, Willem E.
APPLICANT: Grossmann, Angelika
TITLE OF INVENTION: METHODS FOR INCREASING HEMATOPOIETIC CELLS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                   Length 1062;
                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                            47.4%; Score 518.8; DB 2;
99.6%; Pred. No. 1.4e-116;
Live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             East
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-482-212-1
; Sequence 1, Application US/08482212
; Patent No. 6013067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue
CITY: Seattle
               1062 base pairs
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                             Conservative
               LENGTH: 1062 base pai
TYPE: nucleic acid
STRANDEDNESS: double
                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                             Similarity
                                                                                                            ; NAME/KEY: CDS
; LOCATION: 1...1
US-08-484-257-18
                                                                                                                                                                                           Query Match
Best Local Simi
Matches 520;
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APPLICANT: Hagen, Frederick S.
APPLICANT: Hagen, Frederick S.
APPLICANT: Kaushansky, Kenneth
APPLICANT: Kuijper, Joseph L.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Oort, Pieter J.
TITLE OF INVENTION: Methods for Stimulating Granulocyte/Macrophage Lineage Cells
CORRESPONDENCE ADDRESS:
                                                                          180
                                                                                                                                                                          240
     TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
                      181 CTGCTCCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGGACCAAG 240
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application US/08484257 Patent No. 5989537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HOLLY, Richard D.
APPLICANT: LOK, S1
APPLICANT: Foster, Donald C.
APPLICANT: Hagen, Frederick S.
APPLICANT: Kaushansky, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: ZymoGenetics, Inc. STREET: 1201 Eastlake E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 95-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO:
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 Using Hematopoietic Proteins
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Pred. No. 1.4e-116;
0; Mismatches 2;
                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/347,748
                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/999,927
                                              ADDRESSEE: ZymoGenetics, Inc. STREET: 1201 Eastlake Avenue
                                                                                                                                                                                                                                                                                                                                                     NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 94-
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.48;
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                       FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1062 base pairs
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Best Local Similarity 99.6
Matches 520; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                           ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS)
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 FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 1..1
US-08-999-927-1
                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                            CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 1062;
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Patent No. 6099830
GENERAL INFORMATION:
APPLICANT: Kaushansky, Kenneth
TITLE OF INVENTION: Methods of Stimulating Erythropoiesis
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                  Score 518.8; DB 3;
Pred. No. 1.4e-116;
0; Mismatches 2;
           CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/482,212
                                                                                                                      REFERENCE/DOCKET NUMBER: 95-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6600 ext 6673
TELEFAX: 206-442-6678
                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
                                                                                                                                                                                                                                                                                                                                                                                                      47.48;
                                                                                                                                                                      TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        LENGTH: 1062 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 47.4 Best Local Similarity 99.6 Matches 520; Conservative
                                                                                                                                                                                                                                       nucleic acid
EDNESS: double
                                                             CLASSIFICATION: 514
                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                     LOCATION:
US-08-482-212-1
                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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NAME/KEY: CDS
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PCT-US95-01829-1
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421 GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG 480
                1 ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG 60
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                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HEMATOPOIETIC PROTEIN AND MATERIALS AND TITLE OF INVENTION: METHODS FOR MAKING IT
                                                           481 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGG 522
                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             APPLICANT: US
APPLICANT: 98102
APPLICANT: APPLICANT: University of Washington
APPLICANT: Seattle
                                                                                                                                                                                                     APPLICANT: ZymoGenetics, Inc.
APPLICANT: 1201 Eastlake Avenue East
APPLICANT: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PARKET, GATY E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-12PC
TELECHONE: 206-442-6600 ext 6673
TELEPHONE: 206-442-6609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US94/08806
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                       Sequence 18, Application PC/TUS9408806 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
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; LOCATION: 1..1
PCT-US94-08806-18
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TITLE OF INVENTION: Methods of Stimulating Erythropoiesis
TITLE OF INVENTION: Using Hematopoietic Proteins.
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                               481 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGG 522
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: University of Washington
APPLICANT: Seattle
APPLICANT: WA
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NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 94-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TYPE: nucleic acid
STRANDEDNESS: double
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CLASSIFICATION:
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31-648
ER: 94-13PC
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 94-1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEPHONE: 206-442-6673
                                                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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1201 Eastlake A
Seattle
                                                                                                                                       LENGTH: 1062 base pairs
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.6
Matches 520; Conservative
                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                         NAME/KEY: CDS
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PCT-US95-14932-3
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PCT-US95-16626-3
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APPLICANT:
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                                                     Length 1062;
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APPLICANT: 98102
APPLICANT: 98102
TITLE OF INVENTION: METHOD FOR SECRETING THROMBOPOLETIN
TITLE OF INVENTION: POLYPEPTIDES
CORRESPONDENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                      Score 518.8; DB 5;
Pred. No. 1.4e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGG
                                                                                0; Mismatches
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APPLICANT: 1201 Eastlake Avenue East
APPLICANT: Seattle
APPLICANT: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US95/14932 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application PC/TUS9514932 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: ZymoGenetics, Inc. 1201 Eastlake Avenue
                                                     47.48;
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                                                                                  Conservative
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                                                                Best Local Similarity
Matches 520; Conserv
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  ) LUCALIUM.
PCT-US95-01829-1
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CITY: Se
                                                     Query Match
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61 TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
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APPLICANT: WA
APPLICANT: WA
APPLICANT: USA
APPLICANT: 9102
TITLE OF INVENTION: PURIFIED THROMBOPOLETIN AND METHOD OF
                                            Indels
Score 518.8; DB 5;
Pred. No. 1.4e-116;
0; Mismatches 2;
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LOCATION:
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; LOCATION:
US-08-388-779A-1
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FEATURE:
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NAME/KEY:
                                                                                                  US-08-388-779A-1
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                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 518.8; DB 5;
Pred. No. 1.4e-116;
0; Mismatches 2;
                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US95/16626 FILLING DATE:
                                          ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 94-11PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELERAS: 206-442-6678
TITLE OF INVENTION: MAKING IT NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                       31,648
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SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
                                                                                                                                                                                                                                          CLASSIFICATION: ATTORNEY/AGENT INFORMATION:
                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 99.6
Matches 520; Conservative
                                                                                                                                                                                                                                                                      NAME: Parker, Gary E
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: double
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: 1..1059
PCT-US95-16626-3
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STATE: WA
COUNTRY: U
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Best Local 8
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SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.4%; Score 518.8; DB 1;
99.6%; Pred. No. 1.5e-116;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/388,779A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                              ATREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
IP: 91320-1720
                                                                                                                                                                                                APPLICANT: Elliott, Steven G.
TITLE OF INVENTION: MGDF ANALOGS
WUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
                                                                                                                                       Sequence 1, Application US/08388779A Patent No. 5696250 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: COOK Ph.D., Robert R.
REGISTRATION NUMBER: 31,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 15-FEB-1995
CLASSIFICATION: 536
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 520; Conservative
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99..1094
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             CAACTGGGACCCACTTGCCTCTCATCCCTCTGGGGCAGCTTTCTGGACAGGTCCGTCTC 360
                                                                                                 CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
                                                                                                                                                 GCTCACAAGGATCCCAATGTCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG 480
                                                                                                                                                                                                481 CGTTTCCTGATGCTTGTAGGAGGTCCACCCTCTGCGTACGG 522
                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          APPLICANT: Elliott, Steven G.
TITLE OF INVENTION: MPL LIGAND ANALOGS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/591,070A FILING DATE: 09-FEB-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATE: APPLICATION NUMBER: US 08/388,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/388,779
FILING DATE: 15-FEB-1995
ATORNEY AGENT INFORMATION:
NAME: COOK, ROBERT R
REGISTRATION NUMBER: 31,602
REGISTRATION NUMBER: A-337B
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: AMGEN INC.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08591070A Patent No. 5756083
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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STRANDEDNESS: single
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LOCATION:
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US-08-591-070A-1
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Length 1342;

Score 518.8; DB 1; Pred. No. 1.5e-116;

47.48;

Query Match Best Local Similarity

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APPLICANT: Bartley, Jakob M.
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Boselman, Robert A.
APPLICANT: Boselman, Robert A.
APPLICANT: Hunt, Pamela
APPLICANT: Hunt, Pamela
APPLICANT: Samal, Babru B.
TITLE OF INVENTION: METHODS FOR TREATING MAMMALS WITH
TITLE OF INVENTION: MONO-PEGYLATED PROTEINS THAT STIMULATE MEGAKARYOCYTE
TITLE OF INVENTION: GROWTH AND DIFFERENTIATION
CORRESPONDENCE: 34
CORRESPONDENCE ANDRESS:
ADDRESSEE: AMGEN INC.
                                                                                                                                    455
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Gaps
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Indels
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Mismatches
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24, Application US/08413803
Patent No. 5765581
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1840 DeHavilland Drive CITY: Thousand Oaks
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INCORMATION:
APPLICANT: Bartley, Timothy D.
APPLICANT: Bosenberger, Jakob M.
APPLICANT: Bosenban, Robert A.
APPLICANT: Bosenban, Robert A.
APPLICANT: Hunt, Pamela
APPLICANT: Anstler, Olaf B.
APPLICANT: Samal, Babru B.
TITLE OF INVENTION: MONO-PECYLATED PROTEINS THAT STIMULATE
TITLE OF INVENTION: MEGAKARYCCYTE GROWTH AND DIFFERENTIATION
CORRESPONDENCE. 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 518.8; DB 1; Length 1342;
Pred. No. 1.5e-116;
0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC_DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIELCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/252,628
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,768
FILING DATE: 31-MAR-1994
ATTORNEY AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-290B
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                            Sequence 24, Application US/08321488A
Patent No. 5795569
                                                                                                                                                                                                                                                                                          E: AMGEN INC.
1840 DeHavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                       STREET: 1840 DeHavilland D
CITY: Thousand Oaks
STATE: California
COUNTRY: US
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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nucleic acid
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Matches 520; Conservative
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LOCATION: 36..98
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LOCATION: 5
FEATURE:
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US-08-321-488A-24
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Pred. No. 1.5e-116;
0; Mismatches 2; Indels 0;
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/321,488
FILING DATE: 12-0CT-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/347,780
FILING DATE: 30-NOV-1994
ATTORNEY/AGENT INFORMATION:

NAME: COOK Ph.D., ROBERT R.

REGISTRATION NUMBER: 31,602
REGISTRATION NUMBER: 31,602
REGISTRATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 1142 base pairs

TYPE: nucleic acid
STRANDEDNESS: unknown

NOTOROGGY: unknown

MOTEGING THE MATERIAL TO TOPOLOGY:

MOTEGING THE MATERIAL TO TOPOLOGY: UNknown

MOTEGING THE MATERIAL TO TOPOLOGY: UNknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/252,628
FILING DATE: 31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.48;
99.68;
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Matches 520; Conservative
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LOCATION:
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; LOCATION:
US-08-413-803-24
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Co-administration of Interleukin-3
Mutant Polypeptides with CSF's for Multi-lineage
Hematopoietic Cell Production
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STREET: P. O. Box 5110
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
                    US-08-469-318-67
US-08-468-609A-67
US-08-413-803-26
US-08-321-488A-26
PCT-US95-03776-28
US-08-469-318-84
US-08-469-318-177
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US-08-469-318-75
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APPLICATION NUMBER: PCT/US95/01184
ELLING DATE: 02-FEB-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2789/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/193,373 FILING DATE: 04-FEB-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,045
FILING DATE: 06-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sarah
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 57, Application US/08471045 Patent No. 6060047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T: Bauer, S. C.
T: Braford-Goldberg, S. C.
Caparon, Maire H.
T: Baston, Alan M.
T: Klein, Barbara.K.
T: McKearn, John P.
T: Olins, Peter O.
T: Paik, Kumnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Braitord-Goldberg, APPLICANT: Gaparon, Maire H. APPLICANT: Gaparon, Maire H. APPLICANT: Rein, Barbara K. APPLICANT: Klein, Barbara K. APPLICANT: McRearn, John P. APPLICANT: Paik, Kumnan APPLICANT: Thomas, John W. TITLE OF INVENTION: Go-admin TITLE OF INVENTION: Hematopo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
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  60680
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Sequence 26, Appli
Sequence 26, Appli
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Sequence 3, Appl
Sequence 3, Appli
Sequence 18, Appl
Sequence 11, Appli
Sequence 11, Appli
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1 ATGGAGCTGACTGAATTGCT......TACGCCACCTTGCCCAGCCC 1083
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-469-712A-57

US-08-457-254-3

US-08-48-257-18

US-08-482-212-1

US-08-999-927-1

PCT-US95-08806-18

PCT-US95-14932-3

PCT-US95-16626-3

US-08-81-779A-1

US-08-81-779A-1

US-08-413-803-24

US-08-414-161B-1

US-08-927-855-1
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PCT-US95-03776-26
US-08-330-517-1
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US-08-591-070A-3
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Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                          181 CTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG
                                                                                                                      Length 1059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Bauer, S. C.
APPLICANT: Bauer, S. C.
APPLICANT: Baston, Maire H.
APPLICANT: Caparon, Maire H.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Olins, Peter O.
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Co-administration of Interleukin-3
TITLE OF INVENTION: Hematopoletic Cell Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGTTTCCTGATGCTTGTAGGAGGTCCACCCTCTGCGTCAGGGGTGGC 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co. ADDRESSEE: Corporate Patent Dept. STREET: P. O. Box 5110
                                                                                                                      Score 523.2; DB 3;
Pred. No. 3.1e-118;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 57, Application US/08469712A Patent No. 6093395
                                   STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                      48.3%;
ilarity 99.4%;
Conservative
         LENGTH: 1059 base pairs
TYPE: nucleic acid
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                    Query Match
Best Local Similarity
Matches 525; Conserv
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                                                                            US-08-471-045-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1059;
                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/469,712A FILING DATE: 06-UON-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.3%; Score 523.2; DB 3; ilarity 99.4%; Pred. No. 3.1e-118; Conservative 0; Mismatches 3;
                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 02-FEB-1995
FILING DATE: 02-FEB-1995
APPLICATION NUMBER: 08 08/193,373
FILING DATE: 04-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REFERENCE/DOCKET NUMBER: 34,547
REFERENCE/DOCKET NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2789/2
TELECOMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 1059 DASE PAIRS
                                                                                                              PC-DOS/MS-DOS
                                                                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (gen
                                 ZIP: 60680
COMPUTER READABLE FORM:
                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 525; Conserv
Illinois
                   USA
                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-469-712A-57
                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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241 GCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGGAGTGATGGCAGCACGGGGA 300
                                                                                                  361 CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
                                                                                                                                                                   421 GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LOK, SI
TITLE OF INVENTION: PURIFIED THROMBOPOIETIN AND METHOD OF
TITLE OF INVENTION: MAKING IT
                                                                                                                                                                                                                                      481 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGGTGGC 528
                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,254
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 523.2; DB 2;
Pred. No. 3.1e-118;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                          Forstrom, John W
Lofton-Day, Catherine E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Parker, Gary E
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 94-1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                           RESULT 4
US-08-457-254-3
; Sequence 3, Application US/08457254
; Patent No. 5986049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.3%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1062 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CILL: WA STATE: WA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seattle
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US-08-457-254-3
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
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Pred. No. 3.1e-118;
0; Mismatches 3; Indels 0;
GENERAL INFORMATION:
APPLICANT: FOSter, Donald C.
APPLICANT: Helpel, Mark
APPLICANT: Helly, Richard D.
TITLE OF INVENTION: METHOD FOR SECRETING THROMBOPOLETIN
TITLE OF INVENTION: POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                    ADDRESSEE: ZymoGenetics, Inc. STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,029
                                                                                                                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERKEY, GATY E
REGISTRATION NUMBER: 31-648
REFRENCE/DOCKET NUMBER: 94-1:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6673
                                                                                                Sequence 3, Application US/08347029
Patent No. 5641655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.3%;
ilarity 99.4%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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Best Local Similarity
Matches 525; Conserv
                                                                                                                                                                                                                                                                                                        CITY: Seattle
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LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                       98102
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                                                               RESULT 3
US-08-347-029-3
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APPLICANT: Fibbe, Willem E.
APPLICANT: Grossmann, Angelika
TITLE OF INVENTION: METHODS FOR INCREASING HEMATOPOIETIC CELLS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      ;
                                                                                                                                                                           Length 1062;
                                                                                                                                                                                                      Indels
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                                                                                                                                                                        Score 523.2; DB 2;
Pred. No. 3.1e-118;
0; Mismatches 3;
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1201 Eastlake Avenue East
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MEDIUM TYPE: Floppy disk
COMPUTER: ISHA FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                      48.3%;
             LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                   Query Match
Best Local Similarity 99.45
Matches 525; Conservative
SEQUENCE CHARACTERISTICS
                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                NAME/KEY: CDS
LOCATION: 1..1059
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STREET: 120.
TTY: Seattle
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US-08-484-257-18
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                                                                                    FEATURE
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APPLICANT: Lok, Si
APPLICANT: Lok, Si
APPLICANT: Hagen, Frederick S.
APPLICANT: Hagen, Frederick S.
APPLICANT: Rausbansky, Kenneth
APPLICANT: Kuijper, Joseph L.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Outt, Pleter J.
TITLE OF INVENTION: Methods for Stimulating Granulocyte/Macrophage Lineage Cells
NUMBER OF SEQUENCES: 21
    CATGICCTICACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC 180
                                                                           181 CTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGCCAAG 240
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APPLICATION NUMBER: US/08/484,257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: ZymoGenetics, Inc. STREET: 1201 Eastlake E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 95-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
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INFORMATION FOR SEQ ID NO: 18:
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ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-6
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Pred. No. 3.1e-118;
0; Mismatches· 3;
                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/347,748
                                               ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue Ed
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                        NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 94-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFRAX: 206-442-6673
                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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al Similarity 99.4%;
525; Conservative 0
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EDNESS: double
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                   CORRESPONDENCE ADDRESS:
                 NUMBER OF SEQUENCES:
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 FITLE OF INVENTION:
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US-08-999-927-1
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Best Local S
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Patent No. 6099830
GENERAL INFORMATION:
APPLICANT: Kaushansky, Kenneth
ITLE OF INVENTION: Methods of Stimulating Erythropoiesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGGTGGC 528
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                                                                           ATTORNEY/AGENT INFORMATION:
NAME: PARKEY, GATY E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 95-10
TELEPHONE: 206-442-6600 ext 6673
TELEPHONE: 206-442-6678
                               APPLICATION NUMBER: US/08/482,212 FILING DATE:
                                                                                                                                                                                 TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.4'
Matches 525; Conservative
               CURRENT APPLICATION DATA:
                                                                 CLASSIFICATION: 514
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COUNTRY: US
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421 GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG 480
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                                                                                                                                                                                                                                                                                                                                                             HEMATOPOIETIC PROTEIN AND MATERIALS AND METHODS FOR MAKING IT
                                                            CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGGTGGC 528
                                                                             Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 523.2; DB 5;
Pred. No. 3.1e-118;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                           APPLICANT: University of Washington Seattle
                                                                                                                                                                                              ZymoGenetics, Inc.
1201 Eastlake Avenue East
Seattle
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NAME: PARKEY, GATY E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-12PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6600 ext 6673
TELEPRA: 206-442-6600 ext 6673
                                                                                                                                                                                                                                                                                                                                                                                                                 AUDMESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                       Sequence 18, Application PC/TUS9408806
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99.4%;
Matches 525; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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LOCATION:
PCT-US94-08806-18
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APPLICANT:
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APPLICANT:
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NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGGTGGC 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: University of Washington APPLICANT: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94-09PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 94-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-648
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LENGTH: 1062 base pain
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STRANDEDNESS: double
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MOLECULE TYPE: CDNA
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CLASSIFICATION:
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NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 94-1:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.4%;
Matches 525; Conservative (
  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                            MOLECULE TYPE: CDNA FEATURE:
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LOCATION:
PCT-US95-14932-3
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PCT-US95-16626-3
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                                                  Length 1062;
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                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                  Score 523.2; DB 5;
Pred. No. 3.1e-118;
                                                                            0; Mismatches
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APPLICANT: 1201 Eastlake Avenue East
APPLICANT: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US95/14932
FILING DATE:
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1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application PC/TUS9514932 GENERAL INFORMATION:
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                                              veery match
Best Local Similarity 99.4%;
Matches 525; Conservative (
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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; LOCATION:
PCT-US95-01829-1
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APPLICANT:
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APPLICANT: 1201 Eastlake Avenue East
APPLICANT: Seattle
APPLICANT: WA
APPLICANT: WA
APPLICANT: WA
APPLICANT: USA
APPLICANT: 98102
TITLE OF INVENTION: PURIFIED THROMBOPOIETIN AND METHOD OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGGTGGC 528
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Pred. No. 3.1e-118;
0; Mismatches 3;
94-13PC
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                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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99.4%; Pred. No. 3.1e-118;
live 0; Mismatches 3;
                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16626
                                         ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                           94-11PC
                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PATKET, Gary
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 94-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
     MAKING IT
                                                                                                                                                                                                                                                                                                                                               LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.4
Matches 525; Conservative
                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                            CORRESPONDENCE ADDRESS:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                                Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: CDS
; LOCATION: 1..1
PCT-US95-16626-3
                                                                                          . USA
                                                                                                                                                                                                         FILING DATE:
                                                                                                    98102
                                      ADDRESSEE:
                                                                                        COUNTRY:
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61 TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
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                 481 CGTTTCCTGATGCTTGTAGGAGGTCCACCCTCTGCGTCAGGGGTGGC
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MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,779A
FILING DATE: 15-FEB-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
48.3%; Score 523.2; DB 1;
Best Local Similarity 99.4%; Pred. No. 3.3e-118;
Matches 525; Conservative 0; Mismatches 3;
                                                                                                           Sequence 1, Application US/08388779A
Patent No. 5696250
GENERAL INFORMATION:
                                                                                                                                                              APPLICANT: Elliott, Steven G.
TITLE OF INVENTION: MGDF ANALOGS
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                          ADDRESSEE: AMGEN INC.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: COOK Ph.D., Robert R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1342 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 36..
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LOCATION:
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US-08-388-779A-1
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Best Local S
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525; Conservative
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CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
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                                                                                                                                                                                                         481 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGGTGGC 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Datentin recesse #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/591,070A FILING DATE: 09-FEB-1996 CLASSIFICATION: 435 APPLICATION DATA: APPLICATION NUMBER: US 08/388,779 FILING DATE: 15-FEB-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Elliott, Steven G.
TITLE OF INVENTION: MPL LIGAND ANALOGS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                     US-08-591-070A-1
Sequence 1, Application US/08591070A
Patent No. 5755083
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: COOK, ROBERT R
REGISTRATION NUMBER: 31,602
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INFORMATION FOR SEQ ID NO: 1:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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36..98
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99..1094
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LOCATION:
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Length 1342;

Score 523.2; DB 1; Pred. No. 3.3e-118;

48.38;

Best Local Similarity

Query Match

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APPLICANT: Bogenberger, Jakob M.
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Bosenman, Robert A.
APPLICANT: Hunt, Pamela
APPLICANT: Kinstler, Olaf B.
APPLICANT: Samal, Babru B.
TITLE OF INVENTION: MONO-PEGYLATED PROTEINS THAT STIMULATE MEGAKARYOCYTE
TITLE OF INVENTION: GROWTH AND DIFFERENTIATION
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
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Gaps
                                                                      36 ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCTAACTGCAAGGCTAACGCTG 95
                                           1 ATGGAGCTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG 60
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APPLICATION NUMBER: US/08/413,803
FILING DATE: 30 MAR-1995
3;
Mismatches
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CLASSIFICATION: 435
PROR APPLICATION DATE: APPLICATION DATE: APPLICATION NUMBER: US 08/221,768
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREEF: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
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Patent No. 5766581
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61 TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
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                                                                                             APPLICANT: Bartley, Timothy D.
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Bosselman, Robert A.
APPLICANT: Hunt, Pamela
APPLICANT: Kinstler, Olaf B.
APPLICANT: Samal, Babru B.
TITLE OF INVENTION: MONO-PEGYLATED PROTEINS THAT STIMULATE
TITLE OF INVENTION: MEGRARYOCYTE GROWTH AND DIFFERENTIATION
NUMBER OF SEQUENCES: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURPUTE: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,488A
FILING DATE: 12-OCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/252,628
FILING DATE: 31-MAY-1994
PRIOR APPLICATION NUMBER: US 08/221,768
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 523.2; DB 1;
Pred. No. 3.3e-118;
0; Mismatches 3;
                                    Sequence 24, Application US/08321488A Patent No. 5795569 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      ADDRESSEE: AMGEN INC.
STREEF: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
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Best Local Similarity 99.4%;
Matches 525; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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EDNESS: unknown
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36..98
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; LOCATION:
US-08-321-488A-24
                     US-08-321-488A-24
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Pred. No. 3.3e-118;
0; Mismatches 3;
                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/347,780
FILING DATE: 30 NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOK Ph.D., ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-290D
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1342 base pairs
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/252,628
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
                                                                                APPLICATION NUMBER: US 08/321,488 FILING DATE: 12-OCT-1994
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Best Local Similarity 99.4%;
Matches 525; Conservative (
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99..1097
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36..98
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36..1097
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NAME/KEY:
LOCATION:
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LOCATION:
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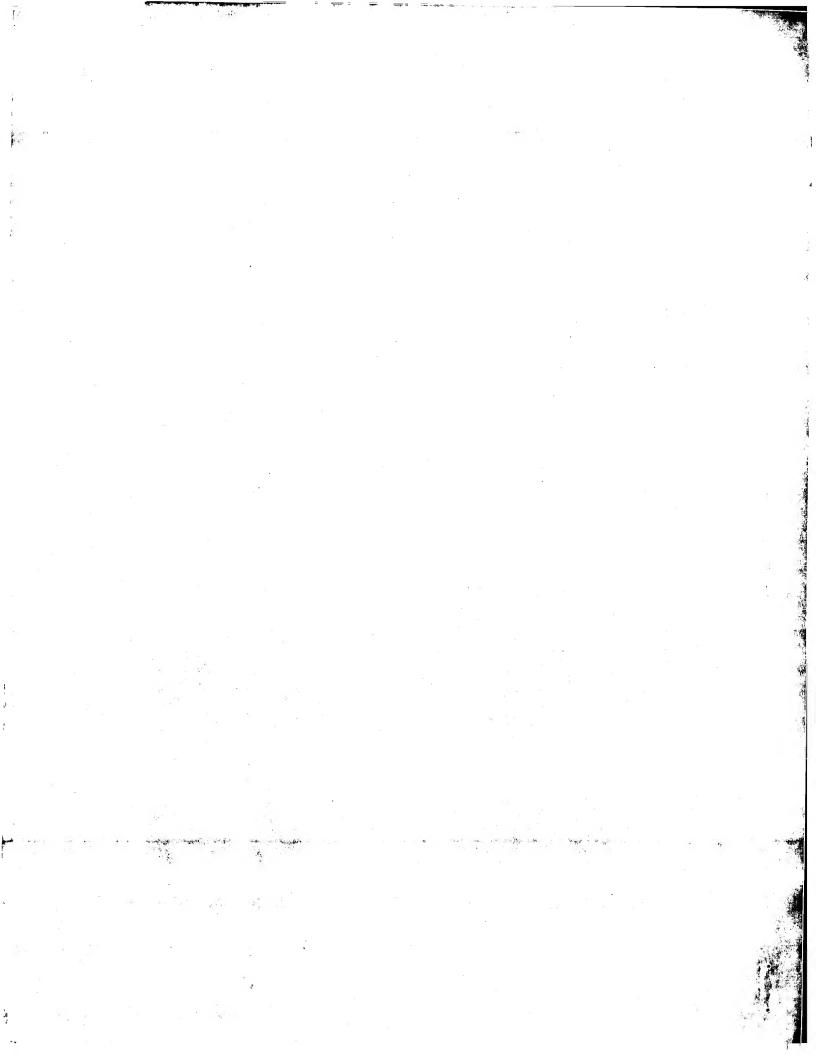
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                                   361 CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
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Search completed: April 5, 2002, 10:34:58 Job time: 4992 sec



Perfect score:

Sequence:

OM nucleic

ou:

Scoring table:

Searched:

Database

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APPLICANT: Thomas, John W.
TITLE OF INVENTION: Co-administration of Interleukin-3
TITLE OF INVENTION: Mutant Polypeptides with CSF's for Multi-lineage
TITLE OF INVENTION: Hematopoietic Cell Production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co. ADDRESSEE: Corporate Patent Dept. STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
                                                                                                US-08-469-318-177
US-08-469-318-178
US-08-468-609A-178
US-08-468-609A-177
PCT-US95-01185-177
PCT-US95-01185-177
US-08-469-318-72
US-08-469-318-78
US-08-469-318-78
US-08-469-318-78
US-08-469-318-78
US-08-469-509A-75
US-08-468-609A-75
US-08-468-609A-75
US-08-468-609A-75
US-08-468-609A-78
US-08-468-609A-78
                                                   US-08-321-488A-26
PCT-US95-03776-28
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APPLICATION NUMBER: PCT/US95/01184
FILING DATE: 02-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/193,373
FILING DATE: 04-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sarah R.
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APPLICATION DATA:
FILING DATE: 06-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bauer, S. C.
Braford-Goldberg, S.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
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REFERENCE/DOCKET NUMBER: C-TELECOMMUNICATION INFORMATION: TELEPHONE: (708)470-6501
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Olins, Peter O.
Paik, Kumnan
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
  SOFTWARE:
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APPLICANT:
APPLICANT:
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APPLICANT:
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US-08-471-045-57
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Sequence 1, Appli
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Sequence 18, Appli
Sequence 1, Appli
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Sequence 18, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-347-029-3
US-08-457-254-3
US-08-484-257-18
US-08-482-212-1
US-08-999-927-1
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US-08-321-488A-24
US-08-414-161B-1
US-08-927-855-1
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PCT-US95-01829-1
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PCT-US95-03776-26
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US-08-388-779A-3
US-08-591-070A-3
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US-08-591-070A-1
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US-08-783-288-1
US-08-890-640-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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                                                                                                                                                               Gaps
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0
                                                                     Length 1059;
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                                                                 Score 526.6; DB 3;
Pred. No. 2.1e-119;
0; Mismatches 4;
      LENGTH: 1059 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-471-045-57
                                                                  50.3%;
99.2%;
                                                               Query Match 50.3
Best Local Similarity 99.2
Matches 529; Conservative
SEQUENCE CHARACTERISTICS
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APPLICANT: Thomas, John W.
TITLE OF INVENTION: Co-administration of Interleukin-3
TITLE OF INVENTION: Mutant Polypoptides with CSF's for Multi-lineage
TITLE OF INVENTION: Hematopoletic Cell Production
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                               G.D. Searle & Co.
                                                                                                    Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maire H.
Baston, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
                                                                                                                                                                                                                                                                                                                                                                                           Dennis A. Bennett, G.D
Corporate Patent Dept.
O. Box 5110
                     Sequence 57, Application US/08469712A Patent No. 6093395 GENERAL INFORMATION:
                                                                                 APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Braford-Goldberg
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
US-08-469-712A-57
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421

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CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGGCGGCGCCCAAC 533

GCTCACAAGGATCCCAATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAGGTG

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61 TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
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                                                                                                                                                                                                                                     CURENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,712A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01184
FILING DATE: 02-FEB-1995
PRIOR APPLICATION NUMBER: US/08/193,373
FILING DATE: 04-FEB-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,547
REFERENCE/POCKET NUMBER: 34,547
RECISTRATION NUMBER: 34,547
RECISTRATION NUMBER: 34,547
REGISTRATION NUMBER: 34,547
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAM: (708)470-6501
THENDALLY COMPANIES OF TO NOTE T
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99.2%; Pred. No. 2.1e-119;
ive 0; Mismatches 4;
                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR EQ. ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1059 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 50.3
Best Local Similarity 99.2
Matches 529; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                     USA
                                                                                                   60680
CITY: Chi
STATE: I]
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-469-712A-57
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CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
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 Gaps
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                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LOK, SI
TITLE OF INVENTION: PURIFIED THROMBOPOIETIN AND METHOD
TITLE OF INVENTION: MAKING IT
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/457,254 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 526.6; DB 2;
Pred. No. 2.1e-119;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ZymoGenetics, Inc. STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                           Forstrom, John W
Lofton-Day, Catherine E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                          RESULT 4
US-08-457-254-3
; Sequence 3, Application US/08457254
; Patent No. 5986049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
ATORNEY/AGENT INFORMATION:
NAME: PATKEY, GATY E
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 94-1
TELECOMMUNICATION INFORMATION:
TELEFAX: 206-442-6673
TELEFAX: 206-442-6673
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
US-08-457-254-3
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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Best Local S
Matches 529,
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                                                                                                                Patent No. Dowlow.

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Heipel, Mark
APPLICANT: Heipel, Mark
APPLICANT: Holly, Richard D.
TITLE OF INVENTION: METHOD FOR SECRETING THROMBOPOIETIN
TITLE OF INVENTION: BOLYPEPTIDES
TITLE OF INVENTION: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.3%; Score 526.6; DB 1; ilarity 99.2%; Pred. No. 2.1e-119; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                     ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                  Sequence 3, Application US/08347029
Patent No. 5641655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 94-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1062 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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Best Local Similarity
Matches 529; Conserv
                                                                                                                                                                                                                                                                                                       Seattle
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                                                                                                                                                                                                                                                                                                                                                        98102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08482212
Patent No. 6013067
GENERAL INFORMATION:
APPLICANT: Fibbe, Willem E.
APPLICANT: Grossmann, Angelika
TITLE OF INVENTION: METHODS FOR INCREASING HEMATOPOIETIC CELLS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGGCGGGGGCCCAAC 533
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Pred. No. 2.1e-119;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: WA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                          50.3%;
                  1062 base pairs
                                                                                                                                                                                          Query Match 50.3
Best Local Similarity 99.2
Matches 529; Conservative
SEQUENCE CHARACTERISTICS
                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                            MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                1..1059
                                                                linear
                                                                                                               NAME/KEY: CDS
                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98102
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LOCATION:
US-08-484-257-18
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APPLICANT: Lok, Si
APPLICANT: Lok, Si
APPLICANT: Lok, Si
APPLICANT: Agen, Frederick S.
APPLICANT: Raushansky, Kenneth
APPLICANT: Kaushansky, Kenneth
APPLICANT: Kijper, Joseph L.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Ort., Pieter J.
TITLE OF INVENTION: Methods for Stimulating Granulocyte/Macrophage Lineage Cells.
                                                                                                                              TCCAGCCCGGCTCCTCCTGTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
                    180
                                                                                   241 GCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGAGTGATGGCAGCACGGGGA 300
                                                                                                                                                                                                                CAACTGGGACCCACTTGCCTCTCATCCCTGGGGCAGCTTTTCTGGACAGGTCCGTCTC 360
                                                                                                                                                                                                                                                                                 CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
                                                                                                                                                                                                                                                                                                                                                                                             GCTCACAAGGAICCCAAIGCCAICTICCTGAGCTICCAACACCTGCTCCGAGGAAAGGIG 480
                                                                121 CATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                            481 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGGCGGGGGCGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/484,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/08484257
Patent No. 5989537
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: ZymoGenetics, Inc. STREET: 1201 Eastlake E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PATKER, GATY E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 95-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEPHONE: 206-442-6678
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-484-257-18
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61 TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAAACTGCTTCGTGACTCC 120
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                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/999,927
   Using Hematopoietic Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 526.6; DB 3;
Pred. No. 2.1e-119;
0; Mismatches 4;
                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/347,748
                                                                                                                                                                                                                                                                                                                                                                           94-09C2
                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                           ADDRESSEE: ZymoGenetics, Inc. STREET: 1201 Eastlake Avenue
                                                                                                                                                                                                                                                                                                                                            NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 94
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.3%;
                                                                                                                                                                                                                                                                                                             FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1062 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99.2
Matches 529; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
EDNESS: double
            NUMBER OF SEQUENCES: 6
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 INVENTION:
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                                                                            Seattle
                                                                                                           USA
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                                                                                                                      ZIP: 98102
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US-08-999-927-1
                                                                                                           COUNTRY:
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STATE:
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TITLE OF INVENTION: Methods of Stimulating Erythropoiesis
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                       50.3%; Score 526.6; DB 3; 99.2%; Pred. No. 2.1e-119;
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                           APPLICATION NUMBER: US/08/482,212
                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6600 ext 6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                        REFERENCE/DOCKET NUMBER: 95-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08999927 Patent No. 6099830 GENERAL INFORMATION:
                                                                                                         31-648
                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-6
                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 529; Conservative
           CURRENT APPLICATION DATA
                                                            CLASSIFICATION: 514
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1..1059
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LOCATION:
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Best Local 8
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NAME/KEY: CDS
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MOLECULE TYPE:
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CITY: Se
STATE: W
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                                                                                                                                                                                                                                                                                                                                       HEMATOPOIETIC PROTEIN AND MATERIALS AND METHODS FOR MAKING IT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 526.6; DB 5;
Pred. No. 2.1e-119;
0; Mismatches 4;
                                                                                                                                                                                                                                                             98102
APPLICANT: University of Washington
Seattle
                                                                                                                                                                                        APPLICANT: ZymoGenetics, Inc.
APPLICANT: 1201 Eastlake Avenue East
APPLICANT: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                2: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                            Sequence 18, Application PC/TUS9408806
GENERAL INFORMATION:
APPLICANT: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REGISCAPOCKET NUMBER: 93-12PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6600 ext 6673
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99.2%;
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TYPE: nucleic acid
STRANDEDNESS: double
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Matches 529; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenet
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CLASSIFICATION:
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LOCATION: 1..1
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CITY: Se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Methods of Stimulating Erythropoiesis TITLE OF INVENTION: Using Hematopoietic Proteins.
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: University of Washington APPLICANT: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application PC/TUS9501829 GENERAL INFORMATION:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: PERKEY BATKET
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 94-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: ZymoGenetics, Inc. STREET: 1201 Eastlake Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: 1062 base pairs
nucleic acid
DEDNESS: double
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TELEPHONE: 206-442-6678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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Query Match 50.3
Best Local Similarity 99.2
Matches 529; Conservative
                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                    1..1059
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                                                                                                                                                       linear
                                                                                                                                                                                          CDS
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                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                             Score 526.6; DB 5;
Pred. No. 2.1e-119;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application PC/TUS9514932
GENERAL INFORMATION:
APPLICANT: ZynoGenetics, Inc.
APPLICANT: 1201 Eastlake Avenue East
APPLICANT: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US95/14932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                           Query Match 50.3%;
Best Local Similarity 99.2%;
Matches 529; Conservative
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; LOCATION:
PCT-US95-01829-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US95-14932-3
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APPLICANT:
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APPLICANT:
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                                             Query Match
Best Local 9
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APPLICANT: 1201 EastLake Avenue East
APPLICANT: Seattle
APPLICANT: WA
APPLICANT: WA
APPLICANT: USA
APPLICANT: BA
APPLICANT BA
APPLICAN
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Pred. No. 2.1e-119;
0; Mismatches 4;
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; Sequence 3, Application PC/TUS9516626
; GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: PAIKEr, GAIY E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 94-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6678
                                                                                                    31-648
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99.2%;
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                                                                                                                      ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16626
FILING DATE:
                                               ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                            94-11PC
                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PARKET, GATY E
REGISTRATION NUMBER: 31,648
REFRENCE/COCKET NUMBER: 94-1:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: MAKING IT NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1062 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 50.3
Best Local Similarity 99.2
Matches 529; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    double
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                                                                              Seattle
                                                                                                            USA
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                                                                                         STATE: WA
COUNTRY: U
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PCT-US95-16626-3
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                      Length 1342;
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COMPUTE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 15-FEB-1995
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                               ADDRESSEE: AMGEN INC.
STREET: 1840 Dehavilland Drive
CTTY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                          APPLICANT: Elliott, Steven G.
TITLE OF INVENTION: MGDF ANALOGS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
                                                                                                                                                ; Sequence 1, Application US/08388779A
; Patent No. 5696250
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: COOK Ph.D., ROBERT R.
REGISTRATION NUMBER: 31,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1342 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36..1094
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MOLECULE TYPE: CDNA
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US-08-388-779A-1
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Gaps

4; Indels

0; Mismatches

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Conservative
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            301 CAACTGGGACCCACTTGCCTCTATCCCTCGGGGCAGCTTTCTGGACAGGTCCGTCTC 360
                                                                                               CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
                                                                                                                                              GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG 480
                                                                                                                                                             Length 1342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,070A
FILING DATE: 09-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/388,779
FILING DATE: 15-FEB-1995
ATTORNEX/AGENT INFORMATION:
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Pred. No. 2.2e-119;
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Elliott, Steven G.
TITLE OF INVENTION: MPL LIGAND ANALOGS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A-337B
                                                                                                                                                                                                                                                                                                                                                                         E: AMGEN INC.
1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08591070A Patent No. 5756083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: A-
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1342 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.3%;
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MEDIUM TYPE: Floppy disk
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99..1094
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36..98
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REGISTRATION NUMBER:
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Best Local Similarity
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STATE: CA
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LOCATION:
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; LOCATION:
US-08-591-070A-1
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US-08-591-070A-1
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APPLICANT: Bartley, Timothy D.
APPLICANT: Boselman, Robert A.
APPLICANT: Bosselman, Robert A.
APPLICANT: Bosselman, Robert A.
APPLICANT: Hunt, Pamela
APPLICANT: Kinstler, Olaf B.
APPLICANT: Samal, Babru B.
TITLE OF INVENTION: METHODS FOR TREATING MAMMALS WITH
TITLE OF INVENTION: MONO-PEGYLATED PROTEINS THAT STIMULATE MEGAKARYOCYTE
TITLE OF INVENTION: GROWTH AND DIFFERENTIATION
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 CATGLCCTTCACAGCAGAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC 215
                                                                                                                                                                                                                                                                                                                                                CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
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                                                                                                       TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
1 ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG 60
                           36 ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCTAACTGCAAGGCTAACGCTG 95
                                                                                                                                                                                                              CATGICCTICACAGGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,768
FILING DATE: 31-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/413,803 FILING DATE: 30-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/08413803
Patent No. 5766581
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: AMGEN INC.
STREET: 1040 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
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MEDIUM TYPE: Floppy disk
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61 TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
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APPLICANT: Bogenberger, Jakob M.
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Hont, Pamela
APPLICANT: Hunt, Pamela
APPLICANT: Kinstler, Oldf B.
TITLE OF INVENTION: MONO-PEGYLATED PROTEINS THAT STIMULATE
TITLE OF INVENTION: MECANARYOCYTE GROWTH AND DIFFERENTIATION
NUMBER OF SEQUENCES: 27
ADDRESSE: AMGEN INC
STREENDERSE: AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AIGGAGCIGACTGAAITGCICCTCGTGGICAIGCTICTCCTAACTGCAAGGCIAACGCTG
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,488A
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 526.6; DB 1;
Pred. No. 2.2e-119;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/252,628
FILING DATE: 31 MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,768
FILING DATE: 31 MAR-1994
ATOMORPAGEN: INFORMATION:
NAME: COOK, ROBETER:
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: 31,602
REPERENCE/DOCKET NUMBER: 31,602
REPERENCE/DOCKET NUMBER: A-290B
INFORMATION FOR SEQ. ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                       Sequence 24, Application US/08321488A
Patent No. 5795569
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                ADDRESSEE: AMGEN INC.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: US
ZIP: 91320-1789
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99.2%;
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TYPE: nucleic acid
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Matches 529; Conservative
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                      US-08-321-488A-24
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; LOCATION;
US-08-321-488A-24
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NAME/KEY:
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PRIOR AFFLICATION DAMER: US OB/252,628
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATE:
APPLICATION DATE:
APPLICATION DATE:
PRIOR APPLICATION DATE:
PRIOR APPLICATION DATE:
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US OB/347,780
FILING DATE: 30-NOY-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOK Ph.D., ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: 31,602
REPRENCE/DOCKET NUMBER: 31,602
SEQUENCE CHARACTER:STICS:
LENGTH 1342 base pairs
TYPE: NUCLGIC acid
TYPE: NUCLGIC acid
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99..1097
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36..98
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LOCATION: 36..
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LOCATION:
FEATURE:
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; LOCATION:
US-08-413-803-24
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Gaps

CATGTCCTTCACAGCAGACTGAGCCAGAGGTTCACCCTTTGCCTACACCTGTC 180

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Title: Perfect score:

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Scoring table:

Searched:

Database

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Homo saplens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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02-SEP-2000 (Rel. 65, Last updated, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                AR087133
AR087571
149760
HUMTHROMB
E16669
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AR087573
185129
D32047
E16668
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AR008878
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HSU59494
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E07164
E15131
I71150
I83709
E09431
                                       E11965
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I05333
I08669
I09205
E01631
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              DB
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1062
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1086
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11721
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11731
11795
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              Length
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  Query
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523.4 b
5221.8 b
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5221.8 b
622.6 b
622.6 b
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                                                                                                                                                                         1 ATGGAGCTGACTGAATTGCT.....TACGCCACCTTGCCCAGCCC 1047
                                                                                         5, 2002, 09:10:07; Search time 2520.15 Seconds
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                            1472140 seqs, 8248589755 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                 nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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E11965 Human cDNA

149760 Sequence 3

185129 Sequence 1 D32047 Homo sapien E16668 cDNA encodi

E11961 Human cDNA I33525 Sequence 1 L33410 Human c-mpl

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JP 1996228781-A/6
10-SEP-1996
14-FEB-1995 JP 1995063298
14-FEB-1994 JP 94P 30900, 25-MAR-1994 JP 94P 79842,
01-JUN-1994 JP 94P 155126, 15-JUN-1994 JP 94P 167328,
01-MOV-1994 JP 94P 304167, 01-DEC-1994 JP 94P 193169,
01-MOV-1994 JP 94P 304167, 01-DEC-1994 JP 94P 298669,
28-DEC-1994 JP 94P 341200
MIYAZARAH HIROSHI, KATO HISASHI, OGAMI KINYA, IWAMATSU AKHIKO,
AKAHORI HIRONORI, KUROKI RYOTA, SHIMIZU TOSHIYUKI,
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           H., Ogami K., Iwamatsu A., Akahori H., Kuroki R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG
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C12N15/09, A61K38/00, C07K14/52, C12N1/21, C12N5/10, C12P21/02,
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Pred. No. 1.6e-99;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 555 BP; 106 A; 183 C; 145 G; 121 T; 0 other;
                                                                                                                                                                                                                                                                              /tissue_type="liver"
1. 555
/product="thrombopoietin"
                  Shimizu T., Muto T.;
"DNA CODING FOR PROTEIN HAVING TPO ACTIVITY";
Patent number JP1996228781-A/6, 10-SEP-1996.
KIRIN BREWERY CO LTD.
                                                                                                                                                                                                                                         Location/Qualifiers
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/organism="Homo
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/db_xref="taxon:9606"
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Best Local Similarity 99.2%;
Matches 529; Conservative 0
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1 (bases 1 to 1059)
Bauer, S. Christopher, Abrams, M.Allen, Braford-Goldberg, S.Ruth,
Bauer, B. Christopher, Abrams, M.Allen, Braford-Goldberg, S.Ruth,
Bauer, B. Christopher, Batton, A. Michael, Klein, B. Kure, McKearn, J. P.,
Coladministration of interleukin-3 mutant polypeptides with CSF's
for multi-lineage hematopoietic cell production
Datent: USC 6093395-A 57 25-JUL-2000;
Location/Qualifiers
1. 1059
361 CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
                             61 TCCAGCCCGGCTCCTCCTGTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
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375 c 236 q
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181 CTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGAGACCAAG 240
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                           1 (bases 1 to 1062)
Holly.R.D., Lok.S., Foster,D.C., Hagen,F.S., Kaushansky,K.,
Kuijper,J.L., Lofton-Day,C.E. and Oort,P.J.
Methods for stimulating granulocyte/macrophage lineage using
                                                                                                                                                                                                                                                                                               1 ATGGAGCTGACTGATTGCTCCTCGTGGTCATCCTTCTCCTAACTGCAAGGCTAACGCTG
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Foster, D.C., Heipel, M.D. and Holly, R.D.
Methods for producing thrombopoletin polypeptides using a
                                                                                                                                                                                                                         Length 1062;
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Patent: US 5641655-A 3 24-JUN-1997;
Location/Qualifiers
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Pred. No. 1.3e-99;
0; Mismatches 4,
                                                                                     thrombopoietin
Patent: US 5989537-A 18 23-NOV-1999
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JS 5641655.
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1. .1062
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481 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGCGGGCCCCCACC 533
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                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                               Unknown.
Unclassified.
1 (bases 1 to 1062)
Forstrom,J.W., Lofton-Day,C.E. and Lok,S.
Purified thrombopoietin and method of making it
Patent: US 5986049-A 3 16-Nov-1999;
Location/Qualifiers
                                                                         PAT
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                                                                                                                                                                                                                                                                                                                                                      Score 526.6; DB 6
Pred. No. 1.3e-99;
0; Mismatches 4
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                                                                      AR087133 1062 bp DNA
Sequence 3 from patent US 5986049.
AR087133
                                                                                                                                                                                                                                                                              /organism="unknown"
1 375 c 236 g
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AR087571
                                                                                                                 AR087133.1 GI:10013899
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99.2%;
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Best Local Similarity
Matches 529; Conserv
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RESULT 4 AR087571

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DEFINITION

Locus

ACCESSION VERSION KEYWORDS SOURCE

/pro/	, tra SPLS SPTC SPTC RFLM LKWDM GTSDY	TSPLI COUNT 223 a 3 N	Query Match Best Local Similarity		1 Argaacraacraarr 61 rccagccggcrccrc	61 TCCAGCCGGCTCCTCC 121 CATGTCCTTCACAGCAG		-	241 GCACAGGACATTCTGGG 	301 CAACTGGGACCCACTTGC	301 CAACTGGGACCCACTTGC		421 GCTCACAAGGATCCCAAT 	481 CGTTTCCTGATGCTTGTA 		ON cDNA encoding thr N E16669 E16669.1 GI:5711	Σ			NIKIN BREWERY CO DOS HOMO Sapiens PN JP 199821224;
		BASE COUNT ORIGIN	Quer	Matches Qy 1	Db Qy	Db Qy	Db 1		Qy 2	Qy	DP 36		Oy 421	Qy 481 Db 481	RESULT E16669 LOCUS	DEFINITION ACCESSION VERSION	SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL	COMMENT
	, o s	. 09	120	180	180 240	240 300	0 0	0 0			_				ii,	L.,				
OUNT 223 a 375 c 236 g 228 t		### ##################################					301 CAACTGGGACCCACTTGCCTCTCATCCCTCTGGGGGAGCTTTCTGGACAGGGGGA 300		CTCCTTGGGGCCCTGCTGGGGCTCCTTGGAACCCAGCTTCCTCCACAGGCAGG	ITTIN	CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGCGGGGGCGCCAAC				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Foster.h C caracter.h C caracter.h C	Holly, R.D., Whitmore, T.E., Heipel, M.D., Bell, L.A.N., Ching, A.F. Human thrombopolein; gene structure. O'Hara, P.J. and Lok, S. Human thrombopolein; gene structure.			1lub. /note="putative" /codon_start=1	/Product≈"thrombopoietin"
BASE COUNT ORIGIN	Quer Best Matc Qy	qa	Oy Dp	Oy 1	Qy 1 Db 1	Oy 2 Db 2	Qy 3(Db 361 Qy 421		Oy 481 Db 481	RESULT	HUMTHROMB LOCUS DEFINITION ACCESSION	VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE	JOURNAL MEDLINE	Source		

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1a; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                      AGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC 180
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                                                                                                                                                                   GAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGA 300
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                                                                                                                     Score 526.6; DB 9; Length 1062;
Pred. No. 1.3e-99;
0; Mismatches 4; Indels 0;
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hrombopoietin.
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243-A/3
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Miyazaki, H., Kato, H., Ogami, K., Iwamatsu, A., Akahori, H., Kuroki, R., Shimizu, T. and Muto, T.
PROTEIN HAVING TPO ACTIVITY
PARENT: JP 1996277296-A 2 22-OCT-1996;
KIRIN BREWERY CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                   MIYAZAKI HIROSHI, KATO HISASHI, OGAMI KINYA, IWAMATSU AKIHIKO,
AKAHORI HIRONORI, KUROKI RYOTA, SHIMIZU TOSHIYUKI, PI MUTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C07K14/52,C07H21/04,C12N15/09,C12P21/02//A61K38/00,(C12P21/02,
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1267)
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25. 1086
/product='thrombopoietin'
Docation/Qualifiers
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Pred. No. 1.3e-99;
0; Mismatches 4;
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 cDNA encoding thrombopoietin.
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/db_xref="taxon:9606"
1 436 c 279 g 27
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(C12P21/02,C12R1:91);
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                                 E12182.1 GI:3251016
JP 1996277296-A/2.
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Best Local Similarity 99.2
Matches 529; Conservative
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SOURCE
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JOURNAL
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                                                                                                                                                                                                                                                                                                 /product "'signal peptide of thrombopoietin' FT
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Pred. No. 1.3e-99;
0; Mismatches 4; Indels 0;
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25. .1086
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Location/Qualifiers
                                                                                                                                                                                                                           /organism='Homo sapiens'/tissue_type='Liver'
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                                                                                                                                                                      Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 386 c 243 g 22
11-AUG-1998
31-JAN-1997 JP 1997019549
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                                                                                            strandedness: Double;
                                                                                                             topology: Linear;
hypothetical: No;
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99.2%;
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Matches 529;
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Query.Match
Best Local Similarity
Matches 529; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RS Miyazaki, H., Kato, H., Ogami, K., Iwamatsu, A., Akahori, H., Kuroki, R.,

RYAZAKI, HAVING TPO ACTIVITY

RININ BREWERY CO LTD

OS Homo sapies (human)

PD 1996291196-A1 05-NOV-1996;

OS Homo sapies (human)

PD 1996291196-A1 05-NOV-1996;

OS HOMO SAPIES (human)

PR 14-FEB-1995 JP 1995355052

PR 14-FEB-1995 JP 1995355052

OI-JUN-1994 JP 94P 155126, 15-JUN-1994 JP 94P 193169, PR

17-AUG-1994 JP 94P 304167, 01-DEC-1994 JP 94P 193169, PR

28-DEC-1994 JP 94P 304167, 01-DEC-1994 JP 94P 298669, PR

PI MIYAZAKI HIRONRI, KATO HISASHI, OGAMI KINYA, IWAMATSU AKIHIKO, TAKANORI HIRONRI, KUROKI RYOTA, SHIMIZU TOSHIYUKI, PI MUTO
325 CAACTGGGACCCACTTGCCTCTATCCTTGGGGCAGCTTTCTGGACAGGTCCGTCTC 384
                    ;
0
                                                              421 GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGGTCGAAGGAAAGGTG 480
                                                                          24-JUN-1998
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/product='thrombopoietin'
25. 87
88. 1083
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Pred. No. 1.3e-99;
0; Mismatches 4;
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Location/Qualifiers
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25. 1086
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Human cDNA encoding thrombopoietin.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
436 c 279 g 271
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JP 1996291196-A/1.
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99.2%;
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Best Local Similarity 99.29
Matches 529, Conservative
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mat_peptide
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FT Source
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61 TCCAGCCGGGTCCTCCTGGTTGTGACCTCCGAGTCCTCAGTAAACTGGTTCGTGACTCC 120
           145 CATGTCCTTCACAGCAGACTGAGCCAGAGGTTCACCCTTTGCCTACACCTGC 204
                                                                              181 CTGCTGCCTGTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG 240
                                                                                         CAACTGGGACCCACTTGCCTCATCCCTGGGGCAGCTTTCTGGACAGGTCCGTCTC 360
                                                                                                                                                                                                 384
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                                     121 CATGICCITCACAGCAGACIGAGCCAGAGGTICACCCTTIGCCIACACCTGIC
                                                                                                                      96 TCCAGCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTGGTGACTCC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
                                                                                                                                                                         121 CATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC 180
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                                                                                                                                                                                                     361 CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACACA
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Pred. No. 1.3e-99;
0; Mismatches 4;
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Sequence 1 from patent US 5756083.
AR008878 1 GI:3967683
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1. 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
454 c 293 g
                                                                                                                                                                                                                                                                                                                                                                                                                             Unclassified.
1 (bases 1 to 1342)
Elliott,s.G.
Mpl ligand analogs
Patent: US 5756083-A 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.3%; S
hilarity 99.2%; P
Conservative 0;
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Qy 361 CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGCCAGGACCACA 420 bb 396 CTCCTTGGGGCCCTGCAGCTCCTTGGAACCCAGCTTCCTCCACAGGCCACAGGACCACA 455 Qy 421 GCTCACAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCAGGGAAAGGTG 480	RESULT 12 AR087573	Mp1 ligand analogs Patent: US 5989538-A 1 23-NOV-1999; Location/Qualifiers in . 134 c 293 g 296 t tch 50.3%; Score 526.6; DB 6; Length 1342; ial Similarity 99.2%; Pred. No. 1.38-99;	AACCHES 529; CONSEIVACIVE U; MISMACCHES 4; INDELS U; Gaps QY 1 ATGGAGCTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG 60	121 CATGLCCTCACAGCAGACTGAGCCAGAGGTTCACCTATGCTACACCTGTC 121 CATGLCCTTCACAGCAGAGCCAGAGGTTCACCCTATGCTACACCTGTC 156 CATGTCCTTCACAGCAGCCAGTGCCCAGAGGTTCACCCTTTGCTACACCTGTC 181 CTGCTGCCTGCTGGACTTTAGCTTGGGAGAAACCCAGATGGAGAGGACAAG 182 CTGCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGAGACCAAG 184 CTGCTGCTGTGGACTTTAGCTTGGGAGATTGGAAAACCCAGATGGAGAGACCAAG 185 CTGCTGCTGTGGACTTTAGCTTGGAGAATGGAAAACCCAGATGGAGAGACCAAG	Oy 241 GCAGGACCATTCTGGGAGCAGTGAGGGAGTGATGGGAGGAGATGATGGGGGA 300 1 11 11 11 11 11 11 11	QY 421 GCTCACAAGGATCCCAATGCCATCTTCCTGAGGTTCCAACACCTGCTCCGAGGAAAGGTG 480 DD 456 GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG 515 QY 481 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGGCGGCGCCCAAC 533 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
OY 241 GCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAG	5-5 5-5	ITION Sequence 24 from patent US 5795569. SION AR023468 AR023468.1 GI:3976762 ED UNROWN. ANISM UNROWN. UNROWN	JOURNAL Datent: US 579569-A 24 18-AUG-1998; FEATURES Location/Qualifiers Source 1. 1342 BASE COUNT 299 a 454 c 293 g 296 t	Query Match Best Local Similarity 99.2%; Pred. No. 1.3e-99; Matches 529; Conservative 0; Mismatches 4; Indels 0; Gaps 0; Qy 1 ArGGAGCTGACTGCATGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGTG 60 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 96 THINININININININININININININININININININ	

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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

Akahori, H., Ohashi, H.,

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/product="thrombopoletin"
/protein_id="BAA21930.1"
/db_xref="di="351118"
/db_xref="di="351118"
/translation="MEITELLLVWLLLTARLTLSSPAPPACDLRVLSKLLRDSHVLH
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GPTCLSSLLGQLSGQVRLLLGALQSLLGTQPTAHKDPMAIFLSFQHLLRGKV
RFLMMLVGGSTLCVRRAPPTAVPSRTSLVTLNBLEDNRTSGLLETNRTFASARTTGSGL
LKWQQGFRATIPGLLNGTFSLDQTPGYLNTHELLNGTRGLFGFPSRRTLGASATTGSGL
LKWQGGFRATICANGTSRSLDQTPGYLNTHELLNGTRGLFGFPSRRTLGAPDISG
GTSDTGSLDPNLQPGYSPSPTHPPTGQYTLFPLPPTLPTPVVQLHPLLPDFSAPTPTP
                                            ogami, K.
Direct Submission
Submitted (08-JUT-1994) to the DDBJ/EMBL/GenBank databases. Kinya
Submitted (08-JUT-1994) to the DDBJ/EMBL/GenBank databases. Kinya
Ogami, KIRIN Brewery Co., Ltd., Pharmaceutical Research Laboratory;
2-2 Soujamachi 1 chome, Maebashi, Gunma 371, Japan
(Tel:0272-54-8618, Fax:0272-52-2307)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG 161
                                                                                                                                                                                                                                                    Erratum:[[published erratum appears in J Biochem (Tokyo) 1996
Jan;119(1):208]]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 TCCAGCCCGGCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 CTGCTGCTGTGTGTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGGAGCAGG
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                                                                                                                                        2 (sites)
Kato,T. Ogami,K., Shimada,Y., Iwamatsu,A., Sohma,Y.,
Horle,K., Kokubo,A., Kudo,Y., Maeda,E., Kobayashi,K.,
Ozawa,T., Inoue,H., Kawamura,K. and Miyazaki,H.
Purification and characterization of thrombopoietin
J. Biochem. 118 (1), 229-236 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 526.6; DB 9;
Pred. No. 1.2e-99;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="liver"
102. 1163
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Best Local Similarity 99.2%;
Matches 529; Conservative
                Mammalia; Eutheria; 1
1 (bases 1 to 1691)
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CDS
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AUTHORS
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JOURNAL
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JOURNAL
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Elliott.S.G.
DNA encoding megakaryocyte growth and development factor analogs
Patent: US 5696250-A 1 09-DEC-1997;
Location/Qualifiers
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Catarrhini; Hominidae; Homo.
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1. .10.
102. .164
/product-'signal peptide of thrombopoietin'
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COMPOSITION CONTAINING THROMBOPOIETIN PROTEIN AND USED FOR STIMULATING RECOVERY OF HEMOSTRATIC THROMBUS-FORMING ABILITY PATENT: JP 1998212243-A 2 11-AUG-1998;
KIRIN BREWERY CO LTD
OS Homo sapiens (human)
PN JP 1998212243-A/2
PD 11-AUG-1998
PP 31-JAN-1997 JP 1997019549
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                               Score 526.6; DB 6; Length 1721; 
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0; Mismatches 4; Indels 0;
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102. .1163
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542 c 371 g 395
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                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1721)
                                                                                                             E16668 1721 bp DNA cDNA encoding thrombopoietin. E16668 E16668 G1:5711351 JP 1998212243-A/2.
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hypothetical: No;
anti-sense: No;
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Search completed: April 5, 2002, 10:29:29 Job time: 4762 sec

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4755.600 Million cell updates/sec
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1047
1 ATGGAGCTGACTGAATTGCT.....TACGCCACCTTGCCCAGCCC 1047
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                               930621 seqs, 428662619 residues
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDSZ/goddata/geneseq/geneseqn/NA1990.DAT:
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Description	Fusion peptide #1	Fusion peptide #2	Fusion peptide #3	Thrombopoletin cod	Human thrombopoiet	Sequence encoding	Human thrombopoiet				
SUMMARIES		AAT41787	AAT41788	AAQ99552	AAT03941	AAT04050	AAT34852	AAT37383	AAT32591	AAT85555	AAV21696
DB	17	17	17	16	16	16	17	17	17	18	19
% Query Match Length DB	1047	1083	1095	861	1062	1062	1062	1062	1062	1062	1062
% Query Match	100.0	94.8	94.3	50.3	50.3	50.3	50.3	50.3	50.3	50.3	50.3
Score	1047	993	987.4	526.6	526.6	526.6	526.6	526.6	526.6	526.6	526.6
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Human thrombopoiet Human thrombopoiet Human MGDF-1 and M Native human mgD 1 Human MGDF-1/2 CDN mhyonyogieticol	Human wild type th Human wild type th Human thrombopolet hML CDNA. Homo sa Human thrombopolet Truncated human mp Truncated human mp	Thrombopoieth cod Plasmid pASN6 enco Plasmid pASN6 enco Plasmid pASN145 en Plasmid pAS28 enco Human megakaryocyt		Sequence encoding Plasmid pp12 contg Sequence of human Human thrombopoiet Human thrombopoiet Human platelet pro Human platelet pro Human platelet-pro Human platelet-pro Human platelet-pro Human MGDF-3. Hom
AAA51991 AAT47958 AAQ99704 AAT10025	AA240191 AA240191 AAQ94107 AAT36658 AAT36658	AAQ09553 AAQ04482 AAQ04484 AAQ04481 AAT33933	AAV29068 AAX32812 AAX41901 AAN70223 AAN71320 AAN60337	AAN81478 AAN91086 AAN71089 AAT41907 AAT41902 AAT29735 AAT29735 AAZ244174 AAZ44179
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526.6 526.6 526.6 526.6	526.6 526.6 526.6 526.6 525	525 514 510.8 506 503.6		486.8 486.8 479.8 478 478 478 478 478
112 114 115	118 20 22 23	22222 242 242 262 263 263 263 263 263 263 263 263 26	2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	8,68,8444444 9,789,000,000,000,000,000,000,000,000,000,0

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RESULT

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Fusion protein; human granulocyte colony stimulating factor; hG-CSF; thrombopoietin; TPO; spacer peptide; blood platelet production; leukocyte production; anaemia; ds.
                                                                                                                                                                                                                                                                                                             Terasaki Y;
                                                                  Fusion peptide #1 having G-CSF and TPO activity.
                                                                                                                                                                                                                                                                                                            Anazawa H, Konishi N, Shiotsu Y, Tamaoki T,
Uchida K, Yamasaki M, Yamashita K, Yokoi H;
                                                                                                                                                 Location/Qualifiers
        AAT41786 standard; DNA; 1047 BP.
                                                                                                                                                                                                                                                                                         (KYOW ) KYOWA HAKKO KOGYO KK.
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64..1047
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                                      Fusion peptide having G-CSF and with thrombopoietin activity - optionally chemically modified with a poly;alkylene glycol, used for
                                                                                                              composed of a peptide having human granulocyte colony stimulating factor (ho.CSF) activity fused with a peptide having thrombopoietin (TPO) activity, opt. via a spacer peptide. Peptides derived from these by deletion, insertion or substitution of one or more amino acid residues are included within the scope of the invention. The fusion peptides stimulate blood platelet and leukocyte production and are useful in the treatment of anaemia.
                                                                                                    The sequences given in AAT41786-88 encode fusion proteins which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGGCGGCGGCGACATATCGC
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                                                                                                                                                                                              Sequence 1047 BP; 192 A; 351 C; 288 G; 216 T; 0 other;
                                                                                 Claim 3; Page 46-48; 71pp; Japanese.
                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 1047; Conservative
                                                            treatment of anaemia
         WPI; 1996-497573/49
                    P-PSDB; AAW00377
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                                                                                                                                                   CTGCAGCTGGACGTCGCCGACTTTGCCACCACCATCTGGCAGCAGCAGAAGAACTGGGA
AGCCAGGCCCTGCAGCTGCAGGCTGCTTGAGCCCAACTCCATAGCGGCCTTTTCCTTAC
                                                                 CAGGGGCTCCTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCACCTTGGACACA
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Yokoi H;
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Yamashita K,
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Uchida K, Yamasaki M,
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P-PSDB; AAW00378.
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(TPO) activity, opt. via a spacer peptide. Peptides derived from these by deletion, insertion or substitution of one or more amino acid residues are included within the scope of the invention. The fusion peptides stimulate blood platelet and leukocyte production and are useful in the treatment of anaemia.
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                                                                             Length 1083;
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                                                   Sequence 1083 BP; 197 A; 355 C; 305 G; 226 T; 0 other;
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                                                                            Score 993; DB 17;
Pred. No. 1.9e-228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAT41786-88 encode fusion proteins which are
                                                       GCCTCCCATCTGCAGAGCTTCCTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAG
GCCACCACCATCTGGCAGCAGATGGAAGTGGGAATGGCCCCTGCCCTGCAGCCCACC
                                            CAGGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGCGCCGGGCAGGGGGGTCCTAGTT
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thrombopoietin; TPO; spacer peptide; blood platelet production;
leukocyte production; anaemia; ds.
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Yamashita K,
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thrombopoietin;
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                                                                                                                                                   CAACTGGGACCCACTTGCCTCTCATCCCTCGGGGCAGCTTTCTGGACAGGTCCGTCTC
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 Length 1095;
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 DB 17;
Score 987.4; DB 17
Pred. No. 4.1e-227
               0; Mismatches
94.3%;
95.5%;
                Conservative
        Similarity
        Best Local Sim
Matches 1046;
 Query Match
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This sequence represents the coding sequence for a thrombopoietin (TPO) protein. TPO is a humoral factor capable of promoting platelet production. The encoded protein can be purified by using a gel affinity
                                                                                                                                                                                                                                                                                                                              Thrombopoietin; TPO; humoral factor; platelet; antibody; therapy; AIDS; thrombocytopenia; hypoplastic anaemia; thrombotic thombocytopenia; disseminated intravascular coagulation syndrome; ds.
1021 ggggtcctagttgcctcccatctgcagagcttcctggaggtgtcgtaccgcgttctacgc 1080
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25..783
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                                                                                                                                                                          mRNA;
                                                                                                                                                                                                                                                                                            Thrombopoietin coding sequence.
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94JP-0167328.
94US-0278083.
94JP-0193169.
94JP-019316.
94US-0320300.
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94US-0361811.
94JP-0341200.
95US-0381478.
94JP-0227159.
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94US-0212164.
94JP-0079842.
94US-0221020.
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25..87
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Kaushansky K;
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          409521626-A1
                                               09-FEB-1995;
                             17-AUG-1995
                                                                         14-FEB-1994
25-FEB-1994
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column where Mp1 has been coupled to a resin. AA099551 and AA099553 also encode TPO proteins. The DNA sequences are inserted into vectors which are used to transform prokaryotic and eukaryotic host cells. Using the proteins encoded by these sequences, and derivatives of them, antibodies specifically immunoreactive with a TPO protein can be created. The antibodies, DNA sequences and vectors are used to isolate the protein sequences. The TPO proteins can then be used in the treatment of platelet disorders. These include thrombocytopenia, hypoplastic anaemia, AIDS, disseminated intravascular coagulation syndrome and
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                                                                                                   Sequence 861 BP; 243 A; 257 C; 197 G; 164 T; 0 other;
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                                                                                                                              Score 526.6; DB 16
Pred. No. 7.2e-117;
0; Mismatches 4;
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99.2%;
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Matches 529; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes human thrombopoietin, which stimulates erythropoiesis to produce an increase in proliferation or differentiation of erythroid cells or to increase reticulocyte counts at least 2-fold over baseline reticulocyte counts and optionally, platelet levels to at least 20000/cu mm. The protein can be used in a composition, optionally with erythropoietin, for use in the treatment of thrombocytopenia and anaemia, such as that caused by destruction of haematopoietic cells in bone marrow, in the treatment of cancer with chemotherapy and radiation, and in pathological conditions such as myelodysplasia, AIDS, aplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC
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Pred. No. 7.5e-117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 38-40; 66pp; English.
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illarity 99.2%;
Conservative 0
                                          94US-0347748.
94US-0196025.
94US-0203197.
94US-0215203.
94US-0288417.
95WO-US01829
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                                                                                                                                                                                                                                                    WASHINGTON
                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-292944/38
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Matches 529; Conserv
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A cDNA clone (AAT34852) codes for human thrombopoietin (AAR98947), a protein that stimulates megakaryopoiesis and thrombocytopoiesis. The cDNA can be incorporated into an expression vector and utilised in the prodn. of low mol. wt. bioactive human thrombopoietin in eukaryotic (partic. yeast or mammalian) host cells. The recombinant
                                                                                                                                                         CTGCTGCCTGCTGTGGGACTTTAGCTTGGGAAATGGAAAACCCAGATGGAGGAGACCAAAG
                                                                                                       CAACTGGGACCCACTTGCCTCTCATCCCTCGTGGGGCAGCTTTCTGGACAGGTCCGTCTC
                                                                                                                                                                                                                                                   CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA
                                      CATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transformed cells, useful for stimulating platelet prodn. esp. treatment of thrombocytopenia
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P-PSDB; AAR98947.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haematopoietic proteins and polypeptides are useful for stimulating platelet production in a mammal when given in a therapeutically effective amount. They are also useful for stimulating bone marrow cell proliferation where the bone marrow cells are megakaryocytes or
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                                                                                                                                                                                                                                                              protein; bone marrow; stem cells; precursor;
                                                              CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGGCGGGGGCGCCAAC
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                                                                                                                                                                                                                                                                                                                                                                    protein.
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Oort PJ;
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; Pred. No. 7.5e-
0; Mismatches
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/*tag= a
/product= Haematopoietic
                                                                                                                                                                                                                                     Sequence encoding haematopoietic protein.
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Lok S, 0
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94US-0196025.
94US-0203197.
94US-0215203.
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99.2%;
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P-PSDB; AAR79906.
                                                                                                                                                                                                                                                                          platelet; therapy;
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14-FEB-1994;
25-FEB-1994;
21-MAR-1994;
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                                                                                     ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG
                                                                                             Thrombopoietin; TPO; aplastic anaemia; congenital cytopaenia; myelodisplatic syndrome; megakaryocytopoiesis; thrombocytopoiesis; haematopoiesis; transgenic animal; ds.
                                                                                                                                                                                                                                                                                                     thrombopoietin has an N-terminus at Ser-22 and a C-terminus betwe Arg-185 and Asn-192 (esp. Arg-198 or Phe-207), and is useful for increasing platelet prodn. in the treatment of thrombocytopenia c
                                                        Score 526.6; DB 17; Length 1062;
Pred. No. 7.5e-117;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                          Sequence 1062 BP; 223 A; 375 C; 236 G; 228 T; 0 other
                       for increasing proliferation of cells in bone marrow.
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99.2%;
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/*tag= a
67..1059
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Best Local Similarity 99.2
Matches 529; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Human thrombopoietin cDNA
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A cDNA clone (AAT37383) codes for human thrombopoietin (TPO) (AAW03512). It was isolated by PCR from human liver and kidney cDNA templates using primers (see also AAT37385-88) derived from exon sequences of a human genomic TPO clone (see also AAT37384) and from the conserved 5' untranslated sequence of mouse TPO cDNA (AAT37382). The cDNA can be used to produce recombinant mature TPO in transformed host cells. Purified, homogeneous TPO is obtd. that is suitable for therapeutic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New pure thrombopoietin free of low mol. wt. degradation prods. useful for treatment of aplastic anaemia, congenital cytopaenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.3%; Score 526.6; DB 17; Length 1062; llarity 99.2%; Pred. No. 7.5e-117; Conservative 0; Mismatches 4; Indels 0;
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                                                                                                                                                                                                                                                                                                           Example 2; Page 63-65; 92pp; English
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    95WO-US16626.
                                                                                                                                   Forstrom JW, Lofton-Day
                                                                                         (ZYMO ) ZYMOGENETICS INC
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CTCCTTGGGGCCCTGCAGGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Increasing haematopoietic cells in patient - by admin. of stem cells from donor previously treated with thrombopoietin, used in patients who have received chemotherapy or radiation for cancer
                                                                                                                                 GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG
                                                                                                                                                                                     TPO; cancer; myeloid cell proliferation; expansion; bone marrow; peripheral blood stem cell; chemotherapy; radiation therapy; breast cancer; leukaemia; lymphoma; multiple myeloma; ds.
                                                                                                                                                                                                                           CGTTICCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGGCGGGGGCCCAAC 533
                                                                                                                                                                                                                                           /product- Thrombopoietin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A cDNA clone (AAT32591) codes for human thrombopoietin (TPO) (AAR99599). Novel DNA constructs code for a secretory peptide (AAR99600) fused to constructs can be expressed in transformed host cells, pref. Pichia pastoris, Saccharomyces cerevisiae or rodent kidney cells, for large-scale, cost-effective prodn. of human TPO, useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA construct encoding native mammalian tissue plasminogen activator secretory peptide and thrombopoietin polypeptide - used to produce thrombopoietin polypeptide(s) on a large scale and in cost effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TCCAGCCGGGTCCTCCTGGTTGTGACCTCCGAGTCCTCAGTAAAGTGCTTCGTGACTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                           Thrombopoietin; TPO; tissue plasminogen activator; cytokine; protein secretion; signal peptide; thrombocytopenia; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 526.6; DB 17; Length 1062;
Pred. No. 7.5e-117;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1062 BP; 223 A; 375 C; 236 G; 228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 41-43; 56pp; English.
                                                                                                                                                                                 Location/Qualifiers
AAT32591 standard; cDNA; 1062 BP.
                                                                                                                                                                                                                                                                                                                                                                                                  Holly RD;
                                                                                                                                                                                                                                                                                                                 95WO-US14932.
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                                                          (first entry)
                                                                              Human thrombopoietin cDNA.
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/*tag= a
64..1059
/*tag= b
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-277784/28.
P-PSDB; AAR99599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 529; Conserv
                                                                                                          Thrombopoietin;
                                                     30-SEP-1996
                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                        WO9617067-A1
                                                                                                                                                                                                                                                                                                              15-NOV-1995;
                                                                                                                                                                                                                                                                                                                                     30-NOV-1994;
                                                                                                                                                                                           sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietin: TPO; expression vector; platelet number; cytokine; human; bone marrow; prolliferation; treatment; cancer; aplastic anaemia; myelodisplastic syndrome; chemotherapy; cytopenia; thrombocytopenia; haematologic disorder; leukaemia; lymphome; ss.
                                                                                                                 TCCAGCCCGGCTCCTCCTGTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
                                                                                                                          CATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC 180
                                                                                                                                                          CAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTT 360
                                                                                                                                                                                                                                                           CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
                                                                                                                                                                                                                                                                                                                    GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG 480
                                                                                                                                                                                                                                                                                                                                    goticacaaggaticocaatgecatoticotgagotitocaacacotgoticogaggaaaggig 480
                                                                 Gaps
This restoration may be further improved by administering TPO to the
                                                                                1 ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG 60
                                                                                                1 atggagctgactgaattgctcctcgtggtcatgcttctcctaactgcaaggctaacgctg 60
         present sequence encodes human TPO.
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                                                 18; Length 1062;
                                                                                                                                                                                                                                                                                                                                                    CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGGCGGCGCCCAAC 533
                                                                                                                                                                                                                                                                                                                                                            4; Indels
                        Sequence 1062 BP; 223 A; 375 C; 236 G; 228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Thrombopoietin polypeptide"
                                                Score 526.6; DB 18;
Pred. No. 7.5e-117;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human thrombopoietin encoding cDNA.
         recipient after transplant. The
                                                                                                                                                                                                                                                                                                                                                                                                            AAV21696 standard; cDNA; 1062
                                               50.3%;
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/product= "
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64..1059
/*tag= c
                                                                Matches 529; Conservative
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                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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This cDNA encodes a thrombopoietin (TPO) polypeptide. This can be used in the construction of a new expression vector replicable in a eukaryotic host cell encoding TPO polypeptides. The vector comprises a transcription promoter, a first DNA segment encoding a secretory leader, a second segment encoding a TPO polypeptide and a transcription terminator which are all operably linked. The second TPO segment consists of cerminator which are all operably linked. The second TPO segment consists of C.T.B. where C is a human TPO cytokine domain, X is a peptide bond or a linker consisting of one or two amino acid residues, such that X along in combination with C or B does not provide a dibasic amino acid pair and B is a polypeptide that can be selected from AAM$3125 to AAW$3126. The secretory leader is a S. cerevisiae alpha-factor secretory leader. B cultured yeast cell containing such an expression vector can be used to cultured yeast cell containing such an expression vector can be used to conjunct the TPO polypeptide can be used to increase proliferation of bone marrow cells for treatment of cytopenia, including those induced by aplastic anaemia, myelodisplastic syndromes, the characteristic containing the used to increase characteristic anaemia, myelodisplastic syndromes, the characteristic chara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietin protein expression vector - used for increasing
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99.2%; Pred. No. 7.5e-117;
ive 0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GR;
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WO9806849-A1
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Sequence 1062 BP; 223 A; 375 C; 236 G; 228 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erthyropoiesis may be stimulated in anaemic mammals by administration of thrombopoietin (TPO), and optionally erythropoietin (EPO). The anaemic mammal to be treated will have shown a haematocrit lavel less than 33 percent of total blood volume, a reticulocyte count of less than 0.8 percent and may have been treated with radiation or chemotherapy. The improved red blood cell level is due to an increase in red blood cell production rather than a decrease in red blood cell destruction. TPO proteins may be used therapeutically to increase proliferation of haematopoietic cells in the bone marrow, such as in the treatment of cytopenia or anaemia, especially associated with bone marrow failure, disorders associated with low red blood cell production, particularly when accompanied by thrombocytopenia and for increasing the level of circulating erythrocytes and erythrocyte precursor cells. TPO and EPO may be used for ex vivo expansion of marrow or peripheral blood progenitor cells.
                                  480
                                                                  480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stimulating erythropoiesis e.g. for treating anemias or cytopenia, or for ex vivo expansion of marrow or peripheral blood progenitor cell, comprises administering thrombopoietin alone or in combination with
361 ctccttggggccctgcagagcctccttggaacccagcttcctccacagggcaggaccaca 420
                                                                                                                                                                                                                                                                                                                                                        Thrombopoletin; TPO; erythropoletin; EPO; erthyropolesis; stimulate; anaemia; radiation; chemotherapy; red blood cell production; haematopoletic cell; cytopenia; ex vivo expansion; anti-anaemic;
                              CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGGCGGGGGCCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 19-22; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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P-PSDB; AAY97136.
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                                                                                CTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG
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/*tag= c
/note= "mature protein residues 1-332"
 21;
Score 526.6; DB 21
Pred. No. 7.5e-117;
0; Mismatches 4;
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25..1086
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• "immature p
Query Match 50.3%;
Best Local Similarity 99.2%;
Matches 529; Conservative
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WPI: 1995-338287/44
P-PSDB; AAR80821, AAR80822, AAR80823, AAR80824, AAR80825, AAR80826
                                                          Mpl ligand; mammalian megakaryocyte growth promoting factor;
                                                                                                                                                     Location/Qualifiers
36..1097
/*tag= a
                                                                              platelet producing factor; ss
                                                                                                                                                                                                                                                                                                                                                   94US-0347780.
94US-0221768.
94US-0252628.
94US-0321488.
                                                                                                                                                                                                                                                                                                                95EP-0104711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bogenberger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Samal BB;
                    Human MGDF-1 and MGDF-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinstler OB,
                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                30-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-1994;
                                                                                                                                                                                                                                                                          04-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TD,
                                                                                                                                                                                                                                    EP675201-A.
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    8, x, c, x, x, d, d, d, d, d, d, d, b, x, b, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCTGCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGAACCAAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAACTGGGACCCACTTGCCTCTCATCCCTGGGGCAGCTTTCTGGACAGGTCCGTCTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCCAGCTTCCTCCACAGGGCAGGACCACA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcacaggacattetgggagcagtgaceettetgetggagggagtgatggeagcagcagggga 324
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                                                                                                                                                                                                                                                                                                                             pref. human serum albumin and/or gelatine, etc., are claimed. The compsns. do not lose TPO activity on storage in a container as the compsn. has reduced adsorption onto the container walls. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGGAGCTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stable thrombopoietin (TPO) compsns. containing TPO and an additive,
                                                                                                                                                                                                             Stable thrombopoietin compositions contains TPO and an additive does not lose thrombopoietin activity on storage in a container
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 17; Length 1086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                             sequence encodes recombinant immature human TPO (1-332).
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1086 BP; 229 A; 386 C; 243 G; 228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 526.6; DB 17;
Pred. No. 7.6e-117;
); Mismatches 4;
                                                                                                                                                                                                                                                                        Example 1; Page 26-28; 38pp; Japanese
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                                      95JP-0056248
96WO-JP00635
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                                                                            BREWERY KK.
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                                                                                                                                                       WPI; 1996-433541/43.
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                                                                                                                                                                           P-PSDB; AAW09314
                                                                            (KIRI ) KIRIN
                                      15-MAR-1995;
                                                                                                                   Otsuki N;
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Mpl ligand is synonymous with MGDF. Mpl ligands are mammalian megakaryocyte growth promoting and/or platelet producing factors. MGDF-2 is a truncated portion of MGDF-1. It is hypothesised that human MGDF is expressed in vivo as a substantially inactive or less active precursor polypeptide that contains variable C-terminal AAs. Upon cleavage of the C-terminal AAs (as well as the signal peptide), the processed form(s) of the molecule retain activity or become more active. It is believed that MGDF-1 may require processing in order to exhibit its activity. The fact that a truncated form MGDF-1 (i.e. MGDF-2) is active supports this hypothesis. Various active molecules that may result from truncations of the sequence set forth as (MGDF-1 (AAR80824) are given in AAR80822, AAR80825, AAR80825. AAR80825 are any of those that have C-terminal truncation variants of MGDF-1 are any of those that have C-terminal truncations from AAR80825.
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the number of megakaryocytes or platelets in patients, e.g. for treating thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
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                                                                                                                                                                               Claim 17; Fig 11; 98pp; English.
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us-09-680-514-4.rng

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concerns analogues of mpl ligand which have altered glycosylation patterns. Alteration of glycosylation of mpl ligand can cause improved biological activity. The mutated protains comprise a lower sialic acid content than wild type mpl ligand. Compositions comprising the mpl ligand analogues of the invention may be used to treat diseases involving an existing or expected megakaryocyte/platelet deficiency, i.e. in thrombocytopaenia.
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         GCACAGGACATICIGGGAGCAGIGACCCTICIGCIGGAGGGAGIGAIGGCAGCACGGGGA 300
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                                                                                                                                                      515
CTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG
                                                              CAACTGGGACCCACTTGCCTCTTCATCCTTGGGGCAGCTTTCTGGACAGGTCCGTCTC
                                                                                             CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA
                                                                                                                                     Native human mpl ligand; altered glycosylation pattern; carbohydrate side chain; sialic acid content; thrombocytopaenia; megakaryocyte/platelet deficiency; ss.
                                                                                                                                                          altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence encodes native human mpl ligand. The invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence with added, deleteduseful in compsns. to treat
                                                                                                                                                                                                                                                                                                                                                    Native human mpl ligand coding sequence.
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
36..1097
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                                                                                                                                                                                                                  AAT36657 standard; cDNA; 1342
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95US-0388779.
                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mpl ligand analogue has glycosylation site(s) - thrombocytopaenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-393399/39.
P-PSDB; AAR99858.
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15-FEB-1995;
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                                                            1 ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG 60
                                                                                                                                                                                                       CTCCTTGGGGCCCTGCAGGCCTCCTTGGAACCCAGCTTCCTCCACAGGCCAGGACCACA 420
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                                                                                                                                 CTGCTGCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG
                                                                                                                                                                            GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACGCTGCTCCGAGGAAAGGTG
                            Score 526.6; DB 17; Length 1342;
Pred. No. 8e-117;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                           481 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGGCGGGGCGCCCAAC 533
Sequence 1342 BP; 299 A; 454 C; 293 G; 296 T; 0 other;
                                               0;
                             50.3%;
                        Query Match 50.3
Best Local Similarity 99.2
Matches 529; Conservative
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Tetraodon Drosophil

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Drosophil

292084 BA WHE0947_C AL572931

Drosophil 602964928 Tetraodon

AL053013 BE480590 AL9615013 AL9615013 AL96159845 BE556176 AL106054 AL106054 AL105377 AL103577 AL10408 AL173312 AL17331 AL17331 AL17331 AL17331 AL17

xr35c05.x hx79f09.x

Tetraodon

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Lo 973)

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El (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI411128 973 bp mRNA EST 14-AUG-2001 602962472F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5118185 5',
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/organism="Mus musculus"
/strain="C2ECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5118185"
                                            BE480590
CNS0091P
                                                                                                                                                                                                    BI345642
CNS0141B
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                                                                                                   5, 2002, 08:51:36 ; Search time 1909.33 Seconds (without alignments) 5892.554 Million cell updates/sec
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BG543320 602575289
BI328788 602984776
BE465194 172130 BA
AI314551 Uj48610.7
AA538257 Vj03007.7
BF789308 602104729
BF78437 208137 MA
BF848766 QV0-EN010
AZ052993 RPCI-23-3
AZ35291 1M0090905
AZ752988 2M0046105
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                                                                                                                                                                   US-09-680-514-4
1047
1 ATGGAGCTGAATTGCT.....TACGCCACCTTGCCCAGCCC 1047
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                  11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
                                                                        nucleic search, using sw model
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BG548320
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AZ3525993
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em_gss_other:*
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Maximum DB seq length: 2000000000
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22.0
113.0
112.9
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301.6
300.6
299.6
285.2
230
135.8
109.4
86.4
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                              Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 295 c 254 g 232 t
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                                                                                                                                                                                                                                                                               962 GCCGGGCAGGAGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTCCTGGAGGTGTCGTACC 1021
                                                                                                                                                                                                                                                               542 CCTCGAGTCTACCACAGAGCTTCCTTTTAAAAAGCTTAGAGCAAGTGAGGAAGATCCAGG 601
                                                                                                                                                                                                                                                                                                                602 GCGATGGCGCAGCGCTCCAGGAGAAGCTGTGCCACCTACAAGCTGTGCCACCCCGAGG 661
                                                                                                                                                                                                                                                                                                                                                                   AGCTGGTGCTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTGAGCAGCTGCCCCA 721
                                                                                                                                                                                                                                                                                                                                                                                722 GCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATAGCGGCCTTTTCCTCTACC 781
                                                                                                                                                                                                                                                                                                                                                                                                                                  782 AGGGGCTCCTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCACCTTGGACACAC 841
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 598)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                               TGCAGCTGGACGTCGCCGACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAA
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                                                                                                                                                                                                                    DB 11; Length 973;
                                                                                                                                                                                                                   Score 320.4; DB 11; Length
Pred. No. 1.8e-62;
0; Mismatches 116; Indels
/clone_lib="NCI_CGAP_Lu33"
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BG548320
BG548320.1 GI:13546985
                                                                                                                                                                                                             Query Match 30.6%;
Best Local Similarity 77.1%;
Matches 390; Conservative
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="InAGE 4703159"
/clone="InAGE 4703159"
/clone="InAE NIH MGC 7"
/lab_host="DHIOB (TI phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_I:
Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5' -CACGGCCATATATGGCC-3' and 3' adaptor sequence:
5' -ATTCTAGAGGCCGAGGCGACATG-7(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1:9
kb (range 0.5-4.0 kb): 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be http://ingage.llnl.gov
Plate: LLCM1541 row: b column: 24
High quality sequence stop: 597.
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602984776F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5137578 5',
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Pred. No. 8.3e-61;
0; Mismatches 2; Indels 0;
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Best Local Similarity 99.4%;
Matches 314; Conservative
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                                                                                                                                                                                                                                                            /organism="Mus musculus"
/Strain="FVBKN"
/db_xref="taxon:10090"
/clone="imAdE:5137578"
/clone_lib="NCI_CGAP_Li9"
/lab_host="nH10B (T1 phage-resistant)"
/lab_host="organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Sterenchologies note: this is a NCI_CGAP Library."
Technologies note: this is a NCI_CGAP Library."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I bases 1 to 900)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 CAACTGGGACCCACTTGCCTCTCATCCCTCGGGGCAGCTTTCTGGACAGGTCCGTCTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGAGCTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-AUG-2000
                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can I found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1338 row: g column: 19
High quality sequence stop: 808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.8%; Score 301.6; DB 11; Length 900; 85.1%; Pred. No. 3.1e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE485194 507 bp mRNA EST 2
172130 BARC 5BOV Bos taurus CDNA 5', mRNA sequence.
BE485194
BE485194.1 GI:9604727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 3.1e-58;
0; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAG 396
                                                                                                                                                                                                                                     Location/Qualifiers
                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   194
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AUTHORS
                                         TITLE
JOURNAL
COMMENT
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VERSION
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/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease
                                                                                                                                        Wells, K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library library (Unpublished (2000)
Contact: Sonstegard TS
                                                                                                                                                                                                                                                                                                                                                        Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                    and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                929
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                                                                 Bovidae; Bovinae; Bos.
1 (bases 1 to 507)
Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCGACTTTGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                870 CACCATCTGGCAGCAGAAGAAGAACTGGGAATGGCCCCTGCCGCGCCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                930 TGCCATGCCGGCCTTCGCCTCTGCTTTCCAGCGCCGGCAGGAGGGGTCCTAGTTGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 300.6; DB 10; Length 507; Pred. No. 4.6e-58;
                                                                                                                                                                                                                                                     USDA, ARS, Beltsville Agricultural Research Center Bd1g, 200 Rm 2A, Beltsville, MD 20705, USA Tel: 301 504 8416
Fax: 301 504 8414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATCTGCAGAGCTTCCTGGAGGTGTCGTACCGCGTTCTACGC 1032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 134 row: J column: 17
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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84.18;
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170 c
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358 CACCTCCTTCACAGCCGACTGAGTCAGTGTCCCGACGTCGACCTTTGTCTATCCCTGTT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA538257.1 GI:2284250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       dq 609
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ORGANISM
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ORIGIN
                                                                                                                                 241
                                                                                                                                                                                                                     301
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JOURNAL
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AA538257
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KEYWORDS
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                                                                                                                                                                                                                                                       (bases 1 to 633)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Lacy, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                    A1314551 633 bp mRNA EST 17-DEC-1998 uj48610.y; Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1923186 5' similar to gb:L34169 Mus musculus thrombopoietin mRNA, complete cds (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 ATGGAGCTGACTGATTTGCTCCTGGCGGCCATGCTTCTTGCAGTGGCAAGACTAACTCTG 297
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                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
Contect: Marra M.Mouse EST Project
Washlo-HHMI Mouse EST Project
Washlington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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nhas 60; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="IMAGE:1923186"
/clone_lib="Sugano mouse liver mlia"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 4.9e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                      The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:979478
Seq primer: custom primer used
High quality sequence stop: 505.
Location/Qualifiers
                                                                                                        AI314551
AI314551.1 GI:4029818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 28.7%;
Best Local Similarity 84.8%;
Matches 336; Conservative
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                                                                                                                                                                           house mouse.
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                                        DEFINITION
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ORGANISM
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VERSION
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AUTHORS
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JOURNAL
COMMENT
AI314551
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 609) Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vj03a07.rl Barstead mouse pooled organs MPLRB4 Mus musculus cDNA clone IMAGE:920628 5' similar to 9b:L34169 Mus musculus thrombopoietin mRNA, complete cds (MOUSE);, mRNA sequence. AA538257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
CAACTGGGACCCACTTGCCTCTCATCCCTCGGGGCAGCTTTCTGGACAGGTCCGTCTC 360
                                                                                                       538 CAGTIGGAACCCTCCTGCCTCTCATCCCTCGGACAGCTNTCTGGGCAGGTTCGCCTC 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:920628"
/clone_lib="Barstead mouse pooled organs MPLRB4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
Contact: Marra MyMouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 492. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              361 CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAG 396
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/dev_stage="7 day"
/lab_host="DH10B"
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/lab_host="DH10B (Tl phage-resistant)"
                                                                                                                                     Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DE 1 (Dases 1 to 878)
National Institutes of Health, Mammalian Gene Collection (MGC)
AL Ontact: Robert Strausberg, Ph.D.
Email: capbb: refmall.nih;gov
Tissue Procurement: Jeffrey E. Green, M.D.
CONA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CONDA Library Preparation: Life Technologies, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9810 row: i column: 08
High quality sequence stop: 628.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF789308 878 bp mRNA EST 12-JAN-2001
602104729F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4222927
                                                                                            TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
                                                                                                                                                   CATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                       -----CCCAGGGCAGGACCACA 583
                                                       Gaps
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                                                     13;
                            Length
                                                     Indels
                          Score 299.6; DB 10;
Pred. No. 8.1e-58;
); Mismatches 69;
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/clone_lib="NCI_CGAP_Kid14"
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/db_xref="taxon:10090"
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BF789308
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                                                 Matches 364;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

1 (bases I to 464)

2 Smith,T.P.L., Grosse, W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. II (4), 626-630 (2001)
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
/note="Organ: kidney; Vector: pcMV-SFORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. |"
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4839
Fax: 402 762 4390
                                                                                                                                                                                                       Score 285.2; DB 11;
Pred. No. 1.6e-54;
0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                           BE754587 464 bp mRNA
208137 MARC 2BOV Bos taurus cDNA
BE754587
BE754587.1 GI:10168579
                                                                                                                                                                                                         27.2%;
84.7%;
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                                                                                                                                                                                                                                                         Conservative
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Sao Paulo-SP,

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/organism="Homo sapiens"
/do.ref="taxon:9606"
/clone_lib="EBN0102"
/clone_lib="EBN0102"
/dev_stage="Adult"
/fouce="Organ: lung_normal; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Gite_2: Smal; A mini-library was made by cloning products
No. 186/16 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cubnA amplification were performed under
low stringency conditions."
61 a 87 c 103 g 76 t
                                                                               Tel: +55-11-2704922
Fax: +55-11-270001
Fax: +55-11-2707001
Fmain sanimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV06t2-QV0-EN0102-Seq primer: puc 18 forward
High quality sequence stop: 327.
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RPCI-23-343116.TJ RPCI-23 Mus musculus genomic clone RPCI-23-343116
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'B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 449)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
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                            Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11;
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89.6%; Pred. No. 8.4e-21
ive 0; Mismatches 1
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Best Local Similarity 89.6
Matches 146; Conservative
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AZ025993
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/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="bH10B"
/note="Vector: pGWV SPORT6; Site_l: Xbal; Site_2: Xhol;
Library made from pooled tissue from testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
a 152 c 128 g 87 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF848766 327 bp mRNA EST 16-JAN-2001
QVO-EN0102-081100-458-906 EN0102 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brio
                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                            Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                Score 230; DB 10;
Pred. No. 4.3e-42;
0; Mismatches 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: AGGAAACAGCTATGACGAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 54 row: J column: 23
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                   /organism="Bos taurus"
                                                                                                 Location/Qualifiers
1. .464
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Laboratory of Cancer Genetics
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22.0%;
Best Local Similarity 85.5%;
Matches 284; Conservative
PCR PRimers
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Gaps

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USA

Length 327;

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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
Cool; Site_2: EcoH; Femala C57Bi_65 mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
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library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://wad.buffalo.edu/conderingframe.htm) or from Resea ch Genetics (info@resqen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html blate: 343 row: I column: 16 Seg primer: SPG Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A2352219 419 bp DNA GSS 29-SEP-ZUUU 1M0090P05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0090P05 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 419)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 GAACAGAGGAAGGCACAGGACATTCTAGGGGCAGTGTCTTTCTACTGGAGGGGGTGTT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 GGCAGCACGAGGACCATCCTCCTCCTCATCCTCGGGACAGCTTTCTGG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 GCAGGTTCGCCTCCTCTTGGGGGCCCTGCAGGAACCCAGGTAAGTCCCCA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 GGCAGCACGGGGACAACIGGGACCCACITGCCTCTCATCCCTCCTGGGGCAGCITICIGG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 ACAGGICCGICTCCTCCTIGGGGCCCTGCAGAGCCTCCTIGGAACCCAGCTICCTCCACA 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
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Pred. No. 1.2e-20;
0; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 t
                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="RPCI-23-343I16"
/clone_lib="RPCI-23"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                              /sex="Female"
/lab_host="DH10B"
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84.4%;
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Matches 152; Conservative
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Fax: 801 585 7177
                                                                                                                                                                                                                         .449
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114) gblAR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 708)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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2M0046105F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0046105 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/G1 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420 AGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACTGCTCCGAGGAAAGGT 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 AGCICACAAGGACCCCAAIGCCCTCTICTIGAGCTIGCAACAACTGCTICGGGGAAAGGI 173
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                                                                                                                                                                                                                                                                                                             /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Llarity 76.6%; Pred. No. 8.4e-15;
Conservative 0; Mismatches 41;
Insert Length: 10000 Std Error: (Plate: 0090 row: P column: 05 Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                High quality sequence stop: 419 Location/Qualifiers
                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC1M0090P05"
                                                                                                                                                                                                                           /strain="C57BL/6J
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                                                                                                                                                                                                                                                                                                                                         /sex="Male"
                                                                                      Class: plasmid ends
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BE377769.1 GI:9323134
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                                                                                                       Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 G 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
8412, USA
Tel: 801 585 506
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/clone="UUGC2MO046I05"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0046 row: I column: 05
Seg primer: CGTFGTAAAACGACGCCAGT
Class: plasmid ends
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
  Unpublished (2000)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 752) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>.</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High Throughput Sequencing Center University of Washington University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Jalde: 3106 row: D column: 7
Seg primer: M13 Reverse
Class: BAC ends
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mahairas GG, Wallace JC, Hood L
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Search completed: April
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/clone=lib="NCI_CGAP_Mam1"
/clssue_type="tumor, blopsy sample"
/dev_stage="a months, virgin"
/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="nort; Vector: pcwV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo osogawa and haron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Wr. The library is named RRCI-98 and was constructed by partial ECORI digestion of Drosophila BNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the pDGP's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNS0091P 925 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                             Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM8767 row: g column: 06
High quality sequence stop: 587.
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Pred. No. 7.4e-05;
0; Mismatches 24
                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fly), genomic survey sequence.
                    Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                         /strain="FVB/N"
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Drosophila melanogaster
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pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               674
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                                                                                                                                                                                                                                                                                                                                                                                Length 925;
                                                                                                                                                                                                                                                                                   others
                                                                                                                                                   /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACRI9D16"
/note="end : TET3"
                                                                                                                                                                                                                                                                                 511
                                                                                                                                                                                                                                                                                                                                                                                5.2%; Score 54.8; DB 13;
15.5%; Pred. No. 0.023;
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66; Conservative 174; Mismatches 182;
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AR103959 Sequence AR087133 Sequence AR087571 Sequence

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14-FEB-1994 JP 94P 39090, 25-MAR-1994 JP 94P 79842, 01-JUN-1994 JP 94P 18900, 25-MAR-1994 JP 94P 79842, 17-MUG-1994 JP 94P 257159, 17-MUG-1994 JP 94P 187159, 17-MUG-1994 JP 94P 187100, MUG-1994 JP 94P 187100, 17-MUG-1994 JP 94P 18710, 17-MUG-1994 JP 94P 187100, 17-
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CI2R1:19),(CI2N5/10,C12R1:91),(C12P21/02,C12R1:19),(C12P21/02,
C12R1:91);
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                  Kato H., Ogami K., Iwamatsu A., Akahori H., Kuroki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GCACAGGACATICTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGGAGGGGA
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Pred. No. 5.9e-99;
3; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 555 BP; 106 A; 183 C; 145 G; 121 T; 0 other;
                               Shimizu T., Muto T.; "DNA CODING FOR PROTEIN HAVING TPO ACTIVITY"; Patent number JP1996228781-A/6, 10-SEP-1996.
KIRIN BREWERY CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="thrombopoietin"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="liver"
1. .555
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topology: Linear;
Location/Qualifiers
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/db_xref="taxon:9606"
/organism="Homo sapiens"
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Best Local Similarity 99.4%;
Matches 525; Conservative
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1996228781-A/6
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                Miyazaki H.,
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1 (bases 1 to 1059)
Bauer, S. Christopher, Abrams, M. Allen, Braford-Goldberg, S.Ruth,
Bauer, S. Christopher, Abrams, M. Allen, Braford-Goldberg, S.Ruth,
Caparon, M. Helena, Easton, A. Michael, Klein, B. Kure, McKearn, J. P.,
Colins, P. O., Paik, K. and Thomas, J.W.
Co-administration of interleukin-3 mutant polypeptides with CSF';
for multi-lineage hematopoietic cell production
Location/Qualifiers
361 CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
                                         14-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCAGCCCGGCTCCTCCTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
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Best Local Similarity 99.4%;
Matches 525; Conservative
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Unclassified.
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ACCESSION VERSION KEYWORDS SOURCE

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61 TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
                         1 (bases 1 to 1062)
Holly,R.D., Lok,S., Foster,D.C., Hagen,F.S., Kaushansky,K.,
Kuijper,J.L., Lofton-Day,C.E. and Oort,P.J.
Methods for stimulating granulocyte/macrophage lineage using
thrombopoletin
Patent: US 5989537-A 18 23-NOV-1999;
                                                                                                                                                                                                                                                                                        241 GCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGGGTGTGGCAGCAGCAGGGG
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Foster, D.C., Heipel, M.D. and Holly, R.D.
Methods for producing thrombopoietin polypeptides using
tissue plasminogen activator secretory peptide
Patent: US 5641655-A 3 24-JUN-1997;
                                                                                                                                                                                                                  Length 1062;
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Pred. No. 5e-99;
0; Mismatches
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Sequence 3 from patent US 5641655.
149760
                                                                                                                                     /organism="unknown"
375 c 236 q
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Local Similarity 99.4%;
nes 525; Conservative (
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                                                                                                                                                                   Unclassified.

1 (bases 1 to 1062)

Forstrom, J.W., Lofton-Day, C.E. and Lok, S.
Purified thrombopoietin and method of making it
Patent: US 5986049-A 3 16-NOV-1999;
Location/Qualifiers
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Pred. No. 5e-99;
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Sequence 3 from patent US 5986049.
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Foster, D.C., Sprecher, C.A., Grant, F.J., Kramer, J.M., Kuijper, J.L., McGrane, V., Hart, C., O'Hara, P.J. and Lok, S. Human thrombopoletin; gene structure, cDNA sequence, expression, and chromosomal localization
                                                                                                                          61 TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
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                                                                                              CATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTTGCCTACACCTGTC
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Human thrombopoletin mRNA, complete
L36052
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    1062
    organism="Homo sapiens"

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L. .1062
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ilarity 99.4%;
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/protein_id="AAC37566.1"
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//translation="MELTELLLVWMLLLTARLTLSSPAPPACDLRVLSKLLRDSHVLH
//translation="MELTELLLVWMLLLTARLTLSSPAPPACDLRVLSKLLRDSHVLH
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1086)
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Pred. No. 5e-99;
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JP 1998212243-A/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.3%;
99.4%;
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JP 1998212243-A/3.
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Homo sapiens
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Best Local Similarity
Matches 525; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1267)

2 Miyazaki, H., Kato, H., Ogami, K., Iwamatsu, A., Akahori, H., Kuroki, R., Shimizu, T. and Muto, T. .

2 Shimizu, T. and Muto, T. .

3 PROTEIN HAVING TPO ACTIVITY

ACTIVITY

Batent: JP 1996277296-A 2 22-OCT-1996;

KIRIN BREWBRY CO LID

OS Homo sapiens (human)

PP 14-FEB-1995 JP 1995161363

PP 14-FEB-1995 JP 1995161363

PP 14-FEB-1995 JP 1995161363

PP 14-FEB-1994 JP 94P 39090, 25-MAR-1994 JP 94P 167328, PR 17-AUG-1994 JP 94P 167328, PR 17-AUG-1994 JP 94P 193169, PR 17-AUG-1994 JP 94P 227159, 17-AUG-1994 JP 94P 193169, PR 28-DEC-1994 JP 94P 241200

DI NOV-1994 JP 94P 341200

PI MIYAZAKI HIROSHI, KATO HISASHI, OGAMI KINYA, IWAMATSU AKIHIKO, PI AKAHORI HIRONORI, KUROKI RYOTA, SHIMIZU TOSHIYUKI, PI MUTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C07K14/52,C07H21/04,C12N15/09,C12P21/02//A61K38/00,(C12P21/02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
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/tissue_type='liver'
25. .1086
/product='thrombopoietin'
25. .87.
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Pred. No. 4.8e-99;
0; Mismatches 3;
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  cDNA encoding thrombopoietin.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1 436 c 279 g 271
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(C12P21/02,C12R1:91);
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Best Local Similarity 99.4%;
Matches 525; Conservative
                                         E12182.1 GI:3251016
JP 1996277296-A/2.
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ORIGIN
  DEFINITION
                                                                                                        ORGANISM
                     ACCESSION
VERSION
KEYWORDS
SOURCE
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JOURNAL
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                                                                                                                                                                      REFERENCE
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                                                                                                                                                                                                                                                                                            25. 87
/product='signal peptide of thrombopoietin' FT
.1086
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                                         KURODA KENJI
A61K38/00,A01N1/02,C07K14/52//C12N15/09,C12P21/02,(C12P21/02,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG 480
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                                                                                                                                                                                                                                                                                                                                                                    /product='thrombopoietin'
25. .1086
                                                                                                                                                                                                                                                                                                                                                                                                                        /product='thrombopoietin'
Location/Qualifiers
                                                                                                                                                                                                                                              /organism='Homo sapiens'
/tissue_type='Liver'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT
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Pred. No. 5e-99;
0; Mismatches 3;
                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .1086
/organism="Homo sapiens"
/db_xref="taxon:9606"
. 386 c 243 g 228
11-AUG-1998
31-JAN-1997 JP 1997019549
                                                                                                  strandedness: Double;
topology: Linear;
hypothetical: No;
anti-sense: No;
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99.48;
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Matches 525; Conservative
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                                                                                   C12R1:19);
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1. .1342
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454 c 293 g
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Sequence 1 from patent US 57
AR008878
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Best Local Similarity 99.4%;
Matches 525; Conservative (
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TITLE
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KEYWORDS
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OS Homo sapiens (human)
PN JP 1996291196-A/1
PD 05-NOV-1996
PR 14-FEB-1995 JP 1995355052
PF 14-FEB-1995 JP 1995355052
PF 14-FEB-1995 JP 1995355052
PF 14-FEB-1995 JP 1995355052
PF 14-FEB-1995 JP 19975126, 15-JUN-1994 JP 94P 79842, PR 14-FEB-1995 JP 1997 227159, 17-AUG-1994 JP 94P 155126, 15-JUN-1994 JP 94P 193169, PR 17-AUG-1994 JP 94P 227159, 17-AUG-1994 JP 94P 227159, 17-AUG-1994 JP 94P 227159, 17-AUG-1994 JP 94P 237159, PR 28-DEC-1994 JP 94P 237159, PR 28-DEC-1994 JP 94P 277159, PR 28-DEC-1994 JP 94P 298669, PR 28-DEC-1994 JP 94P 277159, PR 28-DEC-1994 JP 94P 298669, PR 28-DEC-1994 JP 94P 298669, PR 28-DEC-1994 JP 94P 298669, PR 28-DEC-1994 JP 94P 20869, PR 28-DEC-1994 JP 94P 207159, PR 28-DEC-1994 JP 94P 298669, PR 28-DEC-1994 JP 94P 298669, PR 28-DEC-1094 JP 94P 298669, PR 28-DEC-1994 JP 94P 20869, PR 28-DEC-1994 JP 94P 20869, PR 28-DEC-1094 JP 9
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1 (bases 1 to 1267)

Miyazaki, H., Kato, H., Ogami, K., Iwamatsu, A., Akahori, H., Kuroki, R. Shimzu, T. and Muto, T.

PROTEIN HAVING TPO ACTIVITY.
PROTEIN HAVING TPO ACTIVITY.
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CAACTGGGACCCACTTGCCTCTCATCCCTGGGGCAGCTTTCTGGACAGGTCCGTCTC 384
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                                                                                                                                             421 GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG
                                        361 CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA
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Pred. No. 4.8e-99;
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/organism="Homo
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               CAACTGGGACCCACTTGCCTCTCATCCTCTGGGGCAGCTTTCTGGACAGGTCGTCTC
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                                                              CTGCTGCCTGCTGTGGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG
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Pred. No. 4.7e-99;
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Elliott.S.G.
Mpl ligand analogs
Patent: US 5756083-A 1 26-MAY-1998;
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CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
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Elliott,S.G.
Mpl ligand analogs
Patent: US 5989538-A 1 23-NOV-
Location/Qualifiers
1. 1342
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454 c 293 q
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Best Local Similarity 99.4
Matches 525; Conservative
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Bartley, T.D., Bogenberger, J.M., Bosselman, R.A., Hunt, P.,
Kinstler, O.B. and Samal, B.B.
Mono-pegylated proteins that stimulate megakaryocyte growth differentiation
       CAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTC
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Pred. No. 4.7e-99;
); Mismatches 3
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Location/Qualifiers
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Sequence 24 from patent US:
AR023468
AR023468.1 GI:3976762
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                                                             CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGGTTCCTCCACAGGGCAGGACCACA
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Pred. No. 4.7e-99;
; Mismatches 3;
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Euteleostomi;

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FEATURES

AUTHORS

REFERENCE

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Matches

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Ogami, KTRIN Brewery Co., Ltd., Pharmaceutical Research Laboratory; Cogami, KTRIN Brewery Co., Ltd., Pharmaceutical Research Laboratory; 2-2 Soujamachi 1 chome, Maebashi, Gunma 371, Japan (Tel:0272-54-8618, Fax:0272-52-2307)
2 (sites)
2 (sites)
2 (sites)
3 (sites)
4 (southo, A., Kudo, Y., Iwamatsu, A., Sohma, Y., Akahori, H., Horie, K., Kokubo, A., Kudo, Y., Maeda, E., Kobayashi, K., Ohashi, H., Durification and characterization of thrombopoietin J. Blochem. 118 (1), 229-236 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MELTELLLVVMLLLFARLTLSSPAPPACDLRVLSKLLRDSHVLH
SRLSQCPEVHPLPTPVLLPAVDFSLGEWKTQMEETKAQDILGAVTLLLEGVWAARGQL
GPTCLSSLLGQLSGQVRLLLGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGKV
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LKWOGFRARAT RGLLMQTSRSLDQIPGYLNRTHELLNGTRGLFPGPSRRTLGAPDISS
GTSDTGSLPPNLQPGVSPSPTHPPTGQYTLFPLPPTPTPVYQLHPLLPDPSAPTPTP
TSPLLNTSYTHSQNLSQBG
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Jan;119(1):208]]
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Craniata; Vertebrata; Eutelo
Catarrhini; Hominidae; Homo
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Pred. No. 4.4e-99;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                           /product="thrombopoietin"
/protein_id="BAA21930.1"
/db_xref="G1:2351118"
                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                    /tissue_type="liver"
102. 164
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nes 525; Conservative
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Homo sapiens mRNA for thrombopoietin, complete cds.
D32047 1 G1:2351117
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Patent: US 5696250-A 1 09-DEC-1997;
Location/Qualifiers
                                                 185129 1342 bp DNA
Sequence 1 from patent US 5696250.
185129
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Homo sapiens liver CDNA
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                          48.38;
                                                                                                           GI:3022649
                                                                                                                                                                          Unclassified.
1 (bases 1 to 1342)
Elliott, S.G.
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Homo.
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522 GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAGGT 581
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                                                                                                                                                                                                                                                COMPOSITION CONTAINING THROMBOPOIETIN PROTEIN AND USED FOR STIMULATING RECOVERY OF HEMOSTATIC THROMBUS-FORMING ABILITY Patent: JP 1998212243-A 2 11-AUG-1998;
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                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
1 (bases 1 to 1721)
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/tissue_type='Liver'
1. .101
> 102. .164
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                                 ...1160
/product='thrombopoietin'
102...1163
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/db_xref="taxon:9606"
542 c 371 g 395
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                                                                                                                                                                                                                                                                                              Homo sapiens (human)
JP 198212243-A/2
11-AUG-1998
31-JAN-1997 JP 1997019549
KURODA KENJI
                                                                                                                 E16668 1721 bp DNA cDNA encoding thrombopoietin. E16668 E16668 G1:5711351 JP 1998212243-A/2.
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strandedness: Double;
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hypothetical: No;
anti-sense: No;
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Best Local Similarity 99.4%;
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Human thrombopoiet Human thrombopoiet Human MGDF-1 and M Native human mpl 1 Human MGDF-1/2 cDN

Thrombopoieth cod Human wild type th Human thrombopoiet hML cDNA. Homo sa Human thrombopoiet Truncated human mp Human truncated mp Thrombopoietin cod Plasmid pASN6 enco Plasmid pASN145 en

G-CSF gene isolate Plasmid pBRV2 inse Sequence encoding Plasmid pBRV2 inse Sequence encoding Plasmid pPI2 cont pMONI5937 DNA enco Human interleukin-Sequence of human Human thrombopoiet

Human thrombopoiet Megakaryocyte diff Human platelet pro Human platelet-pro

Terasaki Y;

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Result No.

Human megakaryocyt Nucleotide sequenc Human mpl ligand e Human thrombopoiet

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Searched:

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Fusion protein; human granulocyte colony stimulating factor; hG-CSF; thrombopoietin; TPO; spacer peptide; blood platelet production; leukocyte production; anaemia; ds.
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Uchida K, Yamasaki M, Yamashita K, Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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AAQ04484
AAQ04481
AAQ13933
AAY33933
AAY32812
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AAQ94107
AAT64318
AAT36658
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AAN71320
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Fusion peptide #3
Fusion peptide #1
Thrombopoietin cod
Human thrombopoiet
Sequence encoding
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4919.116 Million cell updates/sec
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                                                                                                                                                                       US-09-680-514-6
1083
1 ATGGAGCTGAATTGCT......TACGCCACCTTGCCCAGCC 1083
                                                                                                         ; Search time 188.75 Seconds
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                    rotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                       930621 seqs, 428662619 residues
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Listing first 45 summaries
                                                                             - nucleic search, using sw model
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                                                              for
                                                                                                                                      composed of a peptide having human granulocyte colony stimulating decror (hot-CEF) activity fused with a peptide having thrombopoietin (TPO) activity, opt. via a spacer peptide. Peptides derived from these by deletion, insertion or substitution of one or more amino acid residues are included within the scope of the invention. The fusion peptides stimulate blood platelet and leukocyte production and are useful in the treatment of anaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGGTGGCGGTTCTGGAGGT
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                                                Fusion peptide having G-CSF and with thrombopoietin activity - optionally chemically modified with a poly:alkylene glycol, used treatment of anaemia
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                                                                                                                            The sequences given in AAT41786-88 encode fusion proteins which
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                                                                                                  Claim 3; Page 49-51; 71pp; Japanese.
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                                                                                                                                         Fusion protein; human granulocyte colony stimulating factor; hG-CSF; thrombopoietin; TPO; spacer peptide; blood platelet production; leukocyte production; anaemia; ds.
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 GGGATCTCCCCCGGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCGACTTT
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                                       TGCTTGAGCCAACTCCATAGCGGCCTTTTCCTCTACCAGGGGCTCCTGCAGGCCCTGGAA
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Uchida K, Yamasaki M,
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Best Local Similarity 97.7%;
Matches 1070; Conservative (
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                                                                                                      GTCGCCGACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCCCCTGCC
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                     Length 1047;
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                     Score 993; DB 17;
Pred. No. 6.8e-228;
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96.28;
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Thrombopoietin; TPO; humoral factor; platelet; antibody; therapy; AIDS;
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                                                                                     mRNA; 861
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                              Thrombopoietin coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kato
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94US-0212164
94US-0221020
94JP-0155126
94US-0278083
94US-0193169
94US-0193169
94US-030300
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94US-0361811.
94JP-0341200.
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94JP-0227159.
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Muto T, Ohgami K, Shimizu
                                                                                    AA099552 standard; cDNA to
                                                                                                                                                 (first entry)
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P-PSDB; AAR81378.
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ccc 1047
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20-JUL-1994;
17-AUG-1994;
18-AUG-1994;
11-OCT-1994;
01-DEC-1994;
                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                 29-APR-1996
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                                                                                                                                                                                                                                                                                                                                                               sig_peptide
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                                                                                                                  AAQ99552;
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                        protein. The is a humoral factor capable of promoting platelet production. The encoded protein can be purified by using a gel affinity column where Mpl has been coupled to a resin. AAQ99551 and AAQ99553 also encode TPO proteins. The DNA sequences are inserted into vectors which are used to transform prokaryotic and eukaryotic host cells. Using the proteins encoded by these sequences, and derivatives of them, antibodies specifically immunoreactive with a TPO protein can be created. The antibodies. DNA sequences and vectors are used to isolate the protein sequences. The TPO proteins can then be used in the treatment of platelet disorders. These include thrombocytopenia, hypoplastic anamemia, AIDS, disseminated intravascular coagulation syndrome and
               sequence for a thrombopoietin (TPO)
                                                                                                                                                                                                                                                                                                                                                                                 TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
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                                                                                                                                                                                                                                                               Score 523.2; DB 16; Length 861;
Pred. No. 9.3e-116;
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                                                                                                                                                                                                                     Sequence 861 BP; 243 A; 257 C; 197 G; 164 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phrombopoietin; erythropoiesis stimulator; treatment;
                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human thrombopoietin coding sequence.
             coding
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                                                                                                                                                                                                                                                              48.3%;
               sequence represents the
                                                                                                                                                                                       thrombotic thrombocytopenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     entitropolesis to produce an increase in proliferation or differentiation of erythroid cells or to increase reticulocyte counts at least 2-fold over baseline reticulocyte counts and optionally, platelet levels to at least 20000/cu mm. The protein can be used in a composition, optionally with erythropoietin, for use in the treatment of thrombocytopenia and anaemia, such as that caused by destruction of haemachooletic cells in bone marrow, in the treatment of cancer with chemotherapy and radiation, and in pathological conditions such as myelodysplasia, AIDS, aplastic
                                                                                                                                                                                                                                                                                                                                                        Stimulation of erythropoiesis using thrombopoietin and opt. erythropoietin - for the treatment of thrombocytopenia and anaemia {\sf ext}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.3%; Score 523.2; DB 16
99.4%; Pred. No. 9.8e-116;
live 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                           sequence encodes human thrombopoietin,
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 38-40; 66pp; English
           Location/Qualifiers
                                                                                                                                               94US-0347748.
94US-0196025.
94US-0203197.
94US-0252491.
94US-0288417.
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                                                                                                                                                                                                                                                                                       (aushansky K;
                                                                WO9521626-A1
                                                                                                                     09-FEB-1995;
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                                    TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC
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and transformed cells, useful for stimulating platelet prodn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haematopoietic proteins and polypeptides are useful for stimulating platelet production in a mammal when given in a therapeutically defective amount. They are also useful for stimulating bone marrow cell proliferation where the bone marrow cells are megakaryocytes or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for in vivo and
         361 ctccttggggccctgcagagcctccttggaacccagcttcctccacagggcaggaccaca
                                                                       GCTCACAAGGATCCCAATGTTCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG
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Pred. No. 9.8e-116;
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                                                                                                                                                                                                                                                                                                   Haematopoiesis; protein; bone marrow; stem cells; precursor;
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                                                                                                                      Indels
                                                                                                           CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haematopoietic proteins and polypeptide(s) - useful \ensuremath{\mathsf{ex}} vivo therapy
                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= Haematopoietic protein.
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                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                AAT04050 standard; cDNA; 1062 BP
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94US-0196025.
94US-0203197.
94US-0215203.
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                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ZYMOGENETICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kuijper JL, Lofton-day
                                                                                                                                                                                                                                                                                                              platelet; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Foster
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21-MAR-1994;
                                                                                                                                                                                                                                                 28-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-AUG-1994;
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14-FEB-1994;
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Matches 525,
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A cDNA clone (AAT34852) codes for human thrombopoietin (AAR98947),

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein that stimulates megakaryopoiesis and thrombocytopoiesis. The cDNA can be incorporated into an expression vector and utilised in the prodn. of low mol.wt. bloactive human thrombopoietin in eukaryotic (partic. yeast or mammalian) host cells. The recombinant thrombopoietin has an N-terminus at Ser-22 and a C-terminus between Arg-185 and Asn-192 (esp. Arg-198 or Phe-207), and is useful for increasing platelet prodn. in the treatment of thrombocytopenia or for increasing proliferation of cells in bone marrow.
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                                                                                                                                                                                                                                                                                                                                                                                 CTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG
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                                                                                                                      Sequence 1062 BP; 223 A; 375 C; 236 G; 228 T; 0 other;
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Pred. No. 9.8e-116;
0; Mismatches 3;
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                                                                                                                                                              Query Match
Best Local Similarity 99.4%;
Matches 525; Conservative
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67..1059
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etc
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congenital cytopaenia,
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Pred. No. 9.8e-116;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                           Sequence 1062 BP; 223 A; 375 C; 236 G; 228
                                                                                                                                                                                                       New pure thrombopoietin free of low mol. v
useful for treatment of aplastic anaemia,
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Best Local Similarity 99.4%;
Matches 525; Conservative
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                                                                     95WO-US16626
                                                                                            94US-0366859
                                                                                                                                                                                                                                           Example 2; Page 63-65;
                                                                                                                    (ZYMO ) ZYMOGENETICS
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                                                                                                                                            Forstrom JW,
                     WO9620955-A1
                                                                     20-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           A cDNA clone (AAT32591) codes for human thrombopoietin (TPO) (AAR995599) Novel DNA constructs code for a secretory peptide (AAR99600) fused to the TPO polypeptide, with a cleavage site at the junction. Such constructs can be expressed in transformed host cells, pref. Pichia pastoris, Saccharomyces cerevisiae or rodent kidney cells, for large-scale, cost-effective prodn. of human TPO, useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                catgtccttcacagcagactgagccagtgcccagaggttcaccctttgcctacacctgtc 180
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                                                                                                           Thrombopoietin; TPO; tissue plasminogen activator; cytokine; protein secretion; signal peptide; thrombocytopenia; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.3%; Score 523.2; DB 17; Length 1062; 99.4%; Pred. No. 9.8e-116; 2ive 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 41-43; 56pp; English.
                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         Holly RD;
                               standard; cDNA; 1062 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombocytopenia.
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64..1059
                                                                     (first entry)
                                                                                        Human thrombopoietin cDNA.
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                                                                                                                                                                                                                                                                                                                         Foster DC, Heipel MD,
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treatment of thro
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In a claimed method, thrombopoietin (TPO) (especially human TPO) is administered to a donor to stimulate proliferation of myeloid cells. Bone marrow or peripheral blood stem cells are collected from the donor and administered to the recipient. The method is used for preparing cells for (bone marrow) transplantation and for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                    Increasing haematopoietic cells in patient - by admin. of stem cells from donor previously treated with thrombopoietin, used in patients who have received chemotherapy or radiation for cancer
421 GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG
                                                                                                                                                                                   301 CAACTGGGACCCACTTGCCTCTCATCCCTCGGGGCAGCTTTCTGGACAGGTCCGTCTC
                                                                                                                                                                                                                                                                                      CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPO; cancer; myeloid cell proliferation; expansion; bone marrow; peripheral blood stem cell; chemotherapy; radiation therapy; breast cancer; leukaemia; lymphoma; multiple myeloma; ds.
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platelet or erythrocyte recovery in a patient receiving chemotherapy or radiation therapy for e.g. breast cancer, leukaemia, lymphoma or multiple myeloma. Treating the donor with TPO accelerates restoration of erythrocyte and thrombocyte levels in the patient after transplant. This restoration may be further improved by administering TPO to the recipient after transplant. The present sequence encodes human TPO.
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                                                                                                                                                                                                 Score 523.2; DB 18;
Pred. No. 9.8e-116;
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This cDNA encodes a thrombopoletin (TPO) polypeptide. This can be used in the construction of a new expression vector replicable in a ewkaryotic host cell encoding TPO polypeptides. The vector comprises a transcription promoter, a first DNA segment encoding a secretory leader, a second segment encoding a TPO polypeptide and a transcription cerminator which are all operably linked. The second TPO segment consists of C-X-B, where C is a human TPO cytokine domain, X is a peptide bond or a linker consisting of one or two amino acid residues, such that X along in combination with C or B does not provide a dibasic amino acid pair and B is a polypeptide that can be selected from AAM53126. The secretory leader is a S. cerevisiae alpha-factor secretory leader. A cultured yeast cell containing such an expression vector can be used to produce the TPO polypeptide. The TPO polypeptide can be used to increase for increasing platelet number in a mammal. It can be used to increase those induced by aplastic anaemia, myelodisplastic syndromes, those induced by aplastic anaemia, myelodisplastic syndromes, thrombocytopenia, haematologic disorders, such as leukaemia and lymphoma
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  caactgggacccacttgcctctcatccctcgggggagctttctggacaggtccgtctc 360
                                 GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG 480
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                                                                                                                                                                                                                                                                                Thrombopoietin; TPO; erythropoietin; EPO; erthyropoiesis; stimulate; anaemia; radiation; chemotherapy; red blood cell production; haematopoietic cell; cytopenia; ex vivo expansion; anti-anaemic; immunomodulator; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stimulating erythropoiesis e.g. for treating anemias or cytopenia, o. for ex vivo expansion of marrow or peripheral blood progenitor cell, comprises administering thrombopoietin alone or in combination with
                      CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA
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/product= Thrombopoietin
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                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..1062
                                                                                                                                                                                          BP
                                                                                                                                                                                        AAA51991 standard; cDNA; 1062
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94US-0335566
                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                           Human thrombopoietin cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNIW ) UNIV WASHINGTON. (ZYMO) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-557618/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAY97136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              erythropoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaushansky K;
                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-1994;
07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-SEP-1997;
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circulating erythrocytes and erythrocyte precursor cells. TPO and EPO I
be used for ex vivo expansion of marrow or peripheral blood progenitor
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                                                                                                                                                                                                                                                                                                                                             TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
                                                                                                                                                                                                                                                                                                                                                                                           61 tecageceggetectectgettgtgacetecgagtecteagtaaactgettegtgaetee 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 CTGCTGCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 ctgctgcctgctgtggactttagcttgggagaatggaaaacccagatggaggagagccaag 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
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                                                                                                                                                                                                         Indels
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/note= "mature protein residues 1-332"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1062 BP; 223 A; 375 C; 236 G; 228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGGTGGC
                                                                                                                                                         Score 523.2; DB 21
Pred. No. 9.8e-116;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human thrombopoietin (1-332) coding sequence.
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/note= "immature protein'
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25..1086
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llarity 99.4%;
Conservative (
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88..1083
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                                                                                                                                                                                   Local Similarity
es 525; Conserv
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mammalian megakaryocyte growth promoting factor;

(first entry)

Location/Qualifiers

36..1097 /*tag= &

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New human megakaryocyte growth and development factor - used to increase the number of megakaryocytes or platelets in patients, e.g. for treating
                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR80821, AAR80822, AAR80823, AAR80824, AAR80825, AAR80826
                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Fig 11; 98pp; English.
                                                                          platelet producing factor; ss
                                              Human MGDF-1 and MGDF-2.
                                                                                                                                                                                                                                                                                                          WPI; 1995-338287/44
                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
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                                                                                             Homo sapiens
                           01-FEB-1996
                                                                                                                                                                                           30-MAR-1995;
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31-MAY-1994;
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                                                               Mpl ligand;
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                                                                                                                                                                                       Stable thrombopoietin (TPO) compsns. containing TPO and an additive, pref. human serum albumin and/or gelatine, etc., are claimed. The compsns. do not lose TPO activity on storage in a container as the compsn. has reduced adsorption onto the container walls. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gctcacaaggatcccaatgccatcttcctgagcttccaaccacctgctccgaggaaaggtg 504
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                            1 ATGGAGCTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG 60
                                                                                                                                         Stable thrombopoietin compositions contains TPO and an additive does not lose thrombopoietin activity on storage in a container
                                                                                                                                                                                                                                                                           Score 523.2; DB 17; Length 1086;
Pred. No. 9.8e-116;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                sequence encodes recombinant immature human TPO (1-332).
                                                                                                                                                                                                                                                 Sequence 1086 BP; 229 A; 386 C; 243 G; 228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGGTGGC
                                                                                                                                                                      Example 1; Page 26-28; 38pp; Japanese.
                                                                                                                                                                                                                                                                              48.38;
                                    96WO-JP00635
                                                      95JP-0056248
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                                                                        (KIRI ) KIRIN BREWERY KK
                                                                                                              WPI; 1996-433541/43.
P-PSDB; AAW09314.
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                                   14-MAR-1996;
WO9628181-A1
                                                      15-MAR-1995;
                 19-SEP-1996
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Matches 525;
                                                                                            Otsuki N;
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Bosselman RA,

Bogenberger JM,

TD,

Samal BB;

94US-0347780. 94US-0221768. 94US-0252628. 94US-0321488.

95EP-0104711

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                                                                                                                                                                                                                                                                                                                                                      MGDF-2) is active supports this hypothesis. Various active molecules that may result from truncations of the sequence set forth as MGDF-1 (AAR80824) are given in AAR80822, AAR80823, & AAR80825. AAR80826 is the signal peptide. The preferred truncation variants of MGDF-1 are any of those that have Crterminal truncations from AA 173.353 (along with cleavage of the signal peptide). The signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tocagoooggotoottotgtgtgacotocgagtcotoagtaaactgcttogtgactoc 155
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Mpl ligand is synonymous with MGDF. Mpl ligands are mammalian megakaryocyte growth promoting and/or platelet producing factors. MGDF-2 is a truncated portion of MGDF-1. It is hypothesised that human MGDF is expressed in vivo as a substantially inactive or less active precursor polypeptide that contains variable C-terminal AAs. Upon cleavage of the C-terminal AAs (as well as the signal peptide), the processed form(s) of the molecule retain activity or become more active. It is believed that MGDF-1 may require processing in order to exhibit its activity. The fact that a truncated form MGDF-1 (i.e.
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Pred. No. 1e-115;
0; Mismatches 3; Indels 0;
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Best Local Similarity 99.4
Matches 525; Conservative
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BP.

AAQ99704 standard; cDNA; 1342

RESULT 14

AAQ99704 ID AA09

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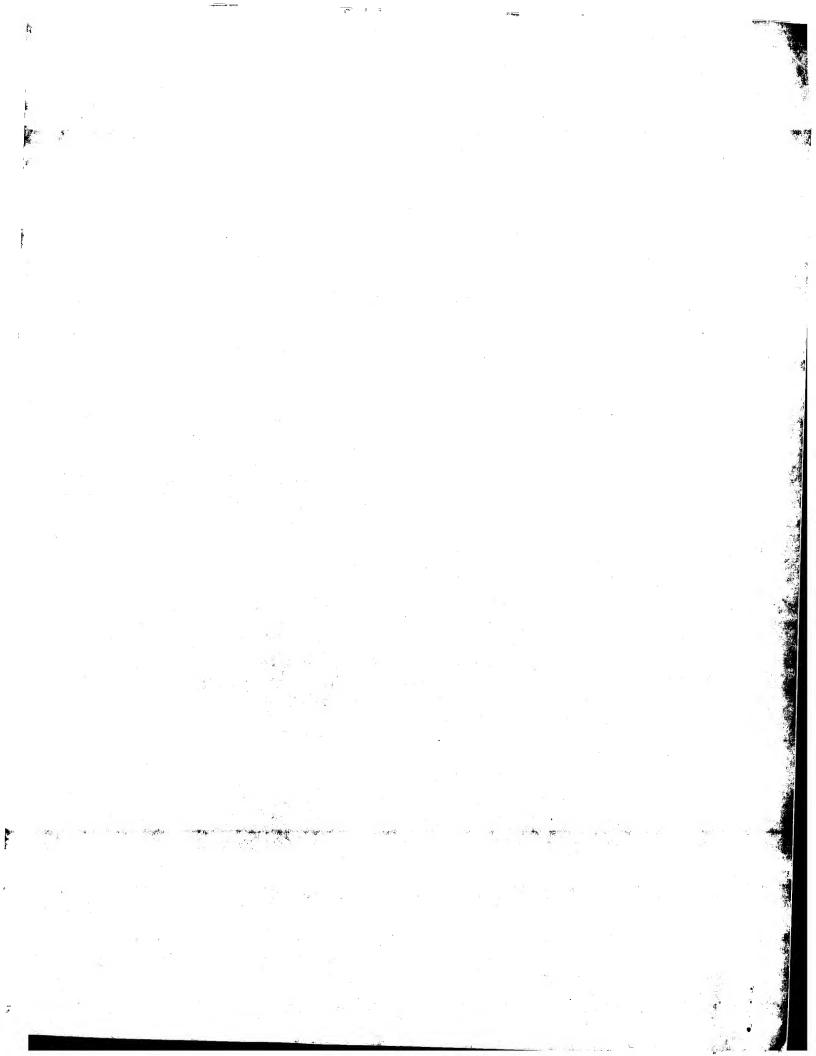
Fig 1; 106pp; English

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Search completed: April Job time: 4950 sec
        Disclosure;
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CTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG
                                CAACTGGGACCCACTTGCCTCTTCCTTGGGGGCAGCTTTCTGGACAGGTCCGTCTC
                                                                                                             CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA
                                                                                                                                GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG
                                                                                                                                                                                                                                                       Native human mpl ligand; altered glycosylation pattern; carbohydrate side chain; sialic acid content; thrombocytopaenia; megakaryocyte/platelet deficiency; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mpl ligand analogue has sequence with added, deleted or altered glycosylation site(s) - useful in compsns. to treat thrombocytopaenia
                                                                                                                                                               CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGGTGGC
                                                                                                                                                                                                                                                                                                      /*tag= a
/product= Full_length_mpl_ligand
36..98
                                                                                                                                                                                                                                          Native human mpl ligand coding sequence.
                                                                                                                                                                                                                                                                                               Location/Qualifiers
36..1097
/*tag= a
                                                                                                                                                                                                     AAT36657 standard; cDNA; 1342
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95US-0388779.
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99..1094
/*tag= c
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15-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence encodes native human mpl ligand. The invention concerns analogues of mpl ligand which have altered glycosylation patterns. Alteration of glycosylation of mpl ligand can cause improved biological activity. The mutated proteins comprise a greater or lesser number of carbohydrate side chains and higher or lower sialic acid content than wild type mpl ligand. Compositions comprising the mpl ligand analogues of the invention may be used to treat diseases involving an existing or expected megakaryocyte/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCTGCCTGCTGTGGACTTTAGCTTGGGAAATGGAAAACCCAGATGGAGGAGACCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctecttgggggccctgcagagcctccttggaacccagcttcctccacagggcaggaccaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG
                                                                                                                                                                                                                                                                                                      Length 1342;
                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                  Sequence 1342 BP; 299 A; 454 C; 293 G; 296 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGGTGGC
                                                                                                                                                                                                                                                                                                 Score 523.2; DB 17;
Pred. No. 1e-115;
0; Mismatches 3;
                                                                                                                                                                                          platelet deficiency, i.e. in thrombocytopaenia
                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                 48.3%;
ilarity 99.4%;
Conservative
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 525; Conserv
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5, 2002, 10:33:11

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Drosophil pat.pk006 PII_84_E1 EMI_68_F0 602728918

zo70d02.s Tetraodon

Drosophil

zl01a10.s zk70f07.s 374523 MA

292084 BA WHE0947_C AL572931

Tetraodon xr35c05.x

hx79f09.x Tetraodon x173e08.x

602964928

Drosophil

hr50h10.x RC3-BT004

wk60c03.x xa42q06.x

xr34c05.x xw63d10.x nbxb0068G wx48h12.x

Perfect score:

Sequence:

OM nucleic

ou:

Run

Scoring table:

Searched:

Database

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National institutes of Health, Mammalian Gene Collection (MCC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. o column: 18
High quality sequence start: 32
High quality sequence stop: 912.
Location/Qualifiers
//organism="mus musculus"
//strain="CZECH II"
//db_xref="taxon:10090"
//clone="IMAGE:5118185"
                                                                                                                                                                                                                                                                                                                          BI411128 973 bp mRNA EST 14-AUG-2001 602962472F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5118185 5', mRNA sequence.
B1411128 I GI:15172051
                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Muses 1 to 973)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
               ALIGNMENTS
                                                                                                                                                                                      CNS022LE
AW193322
BE048584
                                                                                               AA115932
AA058743
BI345642
                                                                                                                      BF868325
BG604563
AL572931
                                                                                                                                                                                                                                       AW273147
AW337946
AQ686347
AI952164
       BE377769
CNS0091P
                                                                                                                                              CNS00720
BI410408
                                                                       AA155632
                                                                                       CNS015Y4
                                                                                                                                                               CNS05709
                               CNS0091P
                                                                BG823538
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VERSION
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AUTHORS
TITLE
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COMMENT
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AA58257 v103a07.r
BE7459308 G02104729
BE74587 208137 MA
BF848766 QV0-EN010
AZ022993 RPCI-23-3
AZ35291 1M0009005
AZ37291 1M0006105
                                                                (without alignments) 6095.163 Million cell updates/sec
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BG548320 602575289
B1328788 602984776
BE485194 172130 BA
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                                                                                               1083
1 ATGGAGCTGACTGAATTGCT......TACGCCACCTTGCCCAGCCC 1083
                                                      April 5, 2002, 09:47:00 ; Search time 1909.33 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                22703874
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                              11351937 seqs, 5372889281 residues
                                                                                                                                                              Total number of hits satisfying chosen/parameters:
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Maximum Match 100%
Listing first 45 summaries
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BG548320
B1328788
BE4828788
BE788257
A7314551
A7314581
BF78988
BF78993
AZ025993
AZ352219
AZ352219
                                        nucleic search, using sw model
                                                                                                                      IDENTITY_NUC Gapox 1.0
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gb_htc:*
gb_gss:*
em_gss_fun:*
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em_gss_rod:*
em_gss_vrt:*
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Maximum DB seq length: 2000000000
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em_gss_pln:*
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2: em_estfum:*
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27.8
27.8
27.7
26.3
26.3
112.5
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8.0
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301.6 300.6 300.6 229.6 285.2 227.8 1135.8 109.2 86.4

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Score

Result Š.

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Unpublished (1999)
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JOURNAL
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BI328788
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            Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " a 295 c 254 g 232 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 598)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG548320 598 bp mRNA EST 04-APR-2001 602575289F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4703159 5'
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                                                                                                                                                                                                                                                                                                     390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTGGTGCTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTGAGCAGCTGCCCCA 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATAGCGGCCTTTTCCTCTACC 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         818 AGGGCTCCTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCACCTTGGACACAC 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451 TGGCCCCTACTGTGCAGCCCACACAGAGCGCCATGCCAGCCTTCACTTCTGCCTTCCAGC 510
                                                                                                                                                                                                                                                                                     578 CCTCGAGTCTACCACAGAGCTTCCTTTTAAAAAGCTTAGAGCAAGTGAGGAAGATCCAGG 637
                                                                                                                                                                                                                                                                                                                                           638 GCGATGCCCAGCGCTCCAGGAGAAGCTGTGTGCCCACCTACAAGCTGTGCCACCCCGAGG 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCAGCTGGACGTCGCCGACTTTGCCACCATCTGGCAGCAGATGGAAGAACTGGGAA 937
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                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                 Score 320.4; DB 11; Length
Pred. No. 1.1e-62;
0; Mismatches 116; Indels
/clone_lib="NCI_CGAP_Lu33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1058 GCGTTCTACGCCACCTTGCCCAGCCC 1083
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BG548320
BG548320.1 GI:13546985
                                                                                                                                                                                                                                tch 29.6%; al Similarity 77.1%; 390; Conservative
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Best Local S:
Matches 390
                                                                                                                                                                          BASE COUNT
ORIGIN
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BG548320
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4703159"
/clone="IMAGE:4703159"
/clone="IMAGE:4703159"
/clone="IM=WIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/note="Grgan: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (gqccqctctgqcc); Site_2: SfiI (gqccattatgqcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAAAGGCCGACAGCGCGCACATGATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAAAGGCCGACAGCGCGCACATGATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAAAGGCCGACATGATGGCC-1' AVENCE in Section Sk (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1541 row: b column: 24
High quality sequence stop: 597.
High quality sequence stop: 597.

Location/Qualifiers
rce
//armais="Homo sapiens"
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602984776F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5137578 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1008 AGGGGTCCTAGTTGCCTCCCATCTGCAGGCTTCCTGGAGGTGTCGTACCGCGTTCTACG 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 CCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTTGGCTTTCCAGCGCCGGGAGG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                768 GCAGCIGGCAGGCTGCTTGAGCCAACTCCATAGCGGCCTTTTCCTCTACCAGGGGCTCCT 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 GCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCCACCTTGGACACACCTGGACACTGGA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 CGTCGCCGACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCCCCTGC 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                888 CGTCGCCGACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACAACTGGGAATGGCCCCTGC
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Pred. No. 5.1e-61;
0; Mismatches 2;
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99.4%;
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Best Local Similarity 99.4°
Matches 314; Conservative
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Similarity
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    ORGANISM
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ORIGIN
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                                                    REFERENCE
                                                            AUTHORS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 900)
HT-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LLAMI1318 row: g column: 19
High quality sequence stop: 808.
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0
                                                                                                                                                                                                                                                                                                                                                                                    Score 301.6; DB 11; Length 900;
Pred. No. 1.9e-58;
0; Mismatches 59; Indels 0;
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BE485194
BE485194.1 GI:9604727
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                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    27.8%;
85.1%;
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Wells,K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Belg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.9809904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib-"BARC 5BOV"
/tissue_type="pooled"
/lab_host="hH108"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                              and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   786 GAGCCAACTCCATAGCGGCCTTTTCCTCTACCAGGGGCTCCTGCAGGCCCTGGAAGGGAT 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            846 CTCCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCGACTTTGCCAC 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             666 GIGIGCCACCIACAAGCIGIGCCACCCCGAGGAGCIGGIGCIGGICGGACACICICIGGG 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        726 CATCCCCTGGGCTCCCCTGAGCAGCTGCCCCAGCCAGGCCTGCAGCTGGCAGGCTGCTT 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                      1 (bases 1 to 507)
Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         906 CACCATCTGGCAGCAGATGGAAGAACTGGCAATGGCCCCTGCCCTGCAGGCCCAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACKWARD: GTTTTCCCAGTCACGACG
Plate: 134 row: J column: 17
Seg primer: ATTTAGGTGACACTATAG.
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1. .507
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                                                                   Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.8%;
84.1%;
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170 c
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126
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                                                                                                                                                                                                                                                  1 (bases 1 to 633)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Marra,M., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                           uj48c10.yl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1923186 5' similar to gb:L34169 Mus musculus thrombopoietin
mRNA, complete cds (MOUSE);, mRNA sequence.
AI314551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 AIGGAGCTGATTTGCTCCTGGCGCCCATGCTTGTTGTGTGCAGTGGCAAGACTAACTCTG 297
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           17-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Pax: 314 286 1810
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .633
/organism="Mus musculus"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                      The Washu-HHMI Mouse EST Project
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High quality sequence stop: 505.
Location/Qualifiers
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/clone="IMAGE:1923186"
                  mRNA
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/lab_host="DH108"
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Matches 336; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
                                                                                                                                                                       house mouse.
                                                                                                                                                                                                                                                                                                                                                                    Waterston, R.
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/lab_host="DH10B (T1 phage-resistant)"
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Matches 320;
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF789308 878 bp mRNA EST 12-JAN-2001
602104729F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4222927
                                                                                        CTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG 240
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                                                                                                                              TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
                                                                                                                                                                                 CATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC 180
                                                                                                                                                                                                                                                                                       CAACTGGGACCCACTTGCCTCTCATCCCTGGGGCAGCTTTCTGGACAGGTCCGTCTC 360
                                                                                                                                                                                                                                                                                                                                                                                                CICCITGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
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                                                                          ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs-rémail.nh.gov.

Tissue Procurement: Jeffery E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

**Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                         13;
                       Score 299.6; DB 10; Length 609;
Pred. No. 5.1e-58;
); Mismatches 69; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4222927"
/clone_lib="NCI_CGAP_Kid14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://image.llnl.gov
Plate: LLAM9810 row: i column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 628.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         CTCTTGGGGGCCCTGCACCGTCCTAAGGAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCACAAGGATCCCAATGCCATCTT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                       27.7%;
ilarity 81.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5', mRNA sequence.
BF789308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
                                     Similarity
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                                      Best Local Sim
Matches 364;
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4356
Fax: 402 762 4390
Fax: 402 762 4390
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Gasas, B., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Bos taurus
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence evaluation of four pooled-tissue normalized bovine cDNA
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                                                                                                                                                                                                                                                                                                                                       TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC
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                                                                                                                                                                    Length 878;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5', mRNA sequence.
                                                                                                                                                                                                              Indels
                                                                                                                                                                  Score 285.2; DB 11;
Pred. No. 1e-54;
); Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208137 MARC 2BOV BOS taurus cDNA
BE754587
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ilarity 84.7%;
Conservative
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Contact: Smith TPL
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61
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Best Local (
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1 (bases I to 327)

1 bases I to 327,

1 of arcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF848766 327 bp mRNA EST 16-JAN-2001
QVO-EN0102-081100-458-906 EN0102 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                   /note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and admetrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 CATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTTGGGGGCCCTGCAGAGCC 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                           203 GCTTGGGAGAATGGAAAACCCAGATGGAGGAGCACCAGGACCACAGGACATTCTGGGAGCAG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 TGACCCTTCTGCTGGAGGGAGTGATGGCAGGGGGACAACTGGGACCCACTTGCCTCT 322
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 TCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGGTCACAAGGATCCCAATGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443 TCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                21.0%; Score 227.8; DB 10; Length 464; 87.2%; Pred. No. 9.7e-42; Live 0; Mismatches 27; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                   FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 54 row: J column: 23
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                        1. .464 //Organism="Bos taurus"
                                                                                                                                               /db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
                                                                                                                                                                                 /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF848766.1 GI:12235903
                                                                                                                                                                                                                                                                                                                                                                                                      Matches 266; Conservative
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PCR PRimers
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VERSION
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/organism="Homo sapiens"

/db_xref="taxon:9606"
/clone_lib==Br00102"
/dev_stage="Adult"
/note="Organ: lung_normal; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A min1-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
61 a 87 c 103 g 76 t
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RPCI-23-343I16.TJ RPCI-23 Mus musculus genomic clone RPCI-23-343I16
, DNA sequence.
AZ025993.1 GI:7101377
                                                                                                    Fax: 455-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-EN0102-
081100-458-000&t3-2000-11-08&t4-1)
Seq primmer: puc lf forward
High quality sequence stop: 327.
Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 449)
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 GGCCCATACACAGGCCCGGCTGTTTGAGCAACTCCATAGCGGGCCTTTTCCTCTACCAGGG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             822 GCTCCTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCACCTTGGACACACTGCA 881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Unbur GSSs: RPCI-23-343116.TV
Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 135.8; DB 11;
Pred. No. 7.1e-21;
0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.5%;
ilarity 89.6%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
CoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

121 c 108 g 129 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bepac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 343 row: I column: 16 Seg primer: SPG Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0090P05R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0090P05 R, DNA sequence.
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Dunn, D., Aoyadi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 GCAGGTTCGCCTCTCTTGGGGGCCCTGCAGGCCTCCTAGGAACCCAGGTAAGTCCCCA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 GGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCTTGGGGGCAGCTTTCTGG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 ACAGGTCCGTCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACA 407
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                                                                                                                                                                                                                                                                          /strain="c57BL/6J"
/db_xref="taxon:10090"
/clone="rec1-23-343116"
/clone=lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
                                                                                                                                                                                                                                                        /organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ352219.1 GI:10431456
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Fax: 801 585 7177
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ORIGIN
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AZ352219/c
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KEYWORDS
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(http://www.ngar.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) (pblART29072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10.Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn,D., Aoyaji,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ792988 708 bp DNA GSS 16-FEB-2001
2M0046105F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0046105 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /note="Weetcr: PWD42nv; Puiffied genomic DNA from M. musculus C57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 CCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCAC 419
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                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Mouse 10kb plasmid UUGC1M library"
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79.6%; Pred. No. 8.3e-15;
tive 0; Mismatches 33; Indels
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Std Error: 0.00
                          Plate: 0090 row: P column: 05
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 419.
                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGC1M0090P05"
                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                       /strain="C57BL/6J'
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Insert Length: 10000
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Matches 129; Conserv
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HS_3106_B1_B04_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3106 Col=7 Row=D, DNA sequence.
AQ888740.1 GI:6344930
                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 CCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CCTGCCTGTGACCCCAGACTCCTAAATAAACTGCTGCGTGACTCCCACCTCCTTCACAGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                        /db.xref="taxon:10090"
/clone="UUGC2M0046105"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86.4; DB 13; Length 708;
Pred. No. 1.4e-09;
0; Mismatches 41; Indels 0
                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0046 row: I column: 05
Seq primer: CGTGTAAAAGGAGGCCAGT
Class: plasmid ends
High quality sequence stop: 708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CGACTGGTGAGCAACCCCAAGCCCCCTGCTTT 152
                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .708
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Best Local Similarity 73.0%;
Matches 111; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male
  Unpublished (2000)
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1 (bases 1 to 752)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus Sukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi. Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 589) (http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                               High Throughput Sequencing Center University of Washington University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 3106 row: D column: 7 Seg primer: M13 Reverse Class: BAC ends
   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606" /clone="Plate=3106 Col=7 Row=D" /clone_lib="CIT Approved Human Genomic Sperm Library D" /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                            Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  509 GAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTAAGTCCAGCCTGCT 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 CCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCAC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                 scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 t
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BE377769
BE377769.1 GI:9323134
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Best Local Similarity
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Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley brosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfiy.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
ECORI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNSO091P 925 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                            DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
plate: LLAMSF67 row: g column: 06
High quality sequence stop: 587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                     Email: cgapbs-r@mail.nih.gov
Lissue Procurement: Gilbert Emith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.1%; Score 65.6; DB 10; Length 589; 76.9%; Pred. No. 7.2e-05; live 0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 rccagcccggcrccrccrgcrrgrgaccrccgagrccrcagraa 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              544 TCCAGCCCGTAGCTCCTGCCTGTGACCCCAGACTCCTAAATAA 587
                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:359885"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
  Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                          /strain="FVB/N"
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Drosophila melanogaster
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Pl and EST libraries. A more detailed description or the state and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             675
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/db_xref="taxon:7227"
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16.1%; Pred. No. 0.015;
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/clone="BACR19D16"
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: April 5, 2002, 10:29:34 ; Search time 2520.15 Seconds (without alignments) 7167.991 Million cell updates/sec	Title: US-09-680-514-8 Perfect score: 1095 Sequence: 1 ATGGAGCTGAATTGCTTACGCCACCTTGCCCAGCCC 1095	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 1472140 segs, 8248589755 residues	Total number of hits satisfying chosen parameters: 2944280	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : GenEmbl:* 1	Dred No is the number of results predicted by chance to have a

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	E02574 DNA encodin E11965 Human cDNA AR103959 Sequence	AR087133 Sequence AR087571 Sequence	I49760 Sequence 3 L36052 Human throm	E16669 cDNA encodi	E12214 Human CDNA	AR023468 Sequence	AR087573 Sequence I85129 Sequence 1	D32047 Homo sapien E16668 cDNA encodi	E11961 Human cDNA	L33410 Human c-mpl	AR008879 Sequence AR087574 Sequence	I85130 Sequence 3	Uliuzo human megak E02575 DNA encodin	U59493 Human throm	E02576 DNA encodin	AR024358 Sequence	E01731 cDNA encodi	E02573 DNA encodin	E15131 Human mRNA	171150 Sequence 1	103/09 Sequence 1 E09431 CDNA encodi	M17706 Human granu	XU3655 Human mKNA E01219 CDNA encodi	105333 Sequence 11	108669 Sequence 1	E01631 DNA encodin	E08529 DNA encodin M13008 Human granu		or derivative.
ID	74 395 395	AR087133 AR087571	I49760	E16669	E12214	AR008878 AR023468	AR087573 I85129	D32047 E16668	E11961	HUMMLCMPL	AR008879 AR087574	185130	HSU11023 E02575	HSU59493	E02576	AR024358	E01731	E02573	E15131	171150	103/09 E09431	HUMGCSF	HSGCSFRI F01219	I05333			E08529 HUMGCSFB	ALIGNMENTS	DNA PAT colony-stimulating factor vasumura, S., Sato, M. and LTD cence; Genes.
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Query Match	47.5	47.4	47.4	47.4	47.4	47.4	47.4						. 6	· •	φ.		. 4	4.	. 4	4.		·	* =		4.		44.3		574 encodi 574 574 1900227 thetic thetic thetic flicial (Misses aki,K., POLYPE POLYPE WA HAKK Artif JP 19
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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14-FBB-1995 JP 1995063298
14-FBB-1995 JP 94P 39090, 25-MAR-1994 JP 94P 79842, 14-FBB-1999 JP 94P 155126, 15-JUN-1994 JP 94P 167328, 17-AUG-1994 JP 94P 193169, 17-AUG-1994 JP 94P 193169, 01-NOV-1994 JP 94P 341200
AINOV-1994 JP 94P 341200
AINOXARI HIROSHI, KUROKI RYOTA, SHIMIZU TOSHIYUK, IWAMATSU AKIHIKO, AKAHORI, HIRONORI, KUROKI RYOTA, SHIMIZU TOSHIYUKI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                C12R1:19), (C12N5/10,C12R1:91), (C12P21/02,C12R1:19), (C12P21/02,
C12R1:91);
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                                                                                                                                                                                                         Miyazaki H., Kato H., Ogami K., Iwamatsu A., Akahori H., Kuroki Shimizu T., Muto T.; Muto T.; Muto T.; Muto Processin Having TPO ACTIVITY"; Patent number JP1996228781-A/6, 10-SEP-1996. KIRIN BREWERY CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                           C12N15/09, A61K38/00, C07K14/52, C12N1/21, C12N5/10, C12P21/02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 106 A; 183 C; 145 G; 121 T; 0 other;
                                     08-OCT-1997 (Rel. 52, Created)
02-SEP-2000 (Rel. 65, Last updated, Version 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="thrombopoietin"
1. .63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.4%; Score 518.8; DB llarity 99.6%; Pred. No. 7e-96; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="liver"
1. .555
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                                                                             Human cDNA encoding thrombopoietin
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Best Local Similarity
Matches 520; Conserv
                                                                                                      JP 1996228781-A/6.
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                                                                                                                                                                                                         /product='human colony-stimulating factor
derivative which
is named 'hG-CSF[ND28]''.
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                                                   C12N9/72, C07K13/00, C07K15/14, C12N1/21, C12N5/10, C12N9/64,
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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SASAKI KATSUTOSHI, NISHI TATSUYA, YASUMURA SHIGEYOSHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGAGCAGCTGCCCAGCCCTGCAGCTGCAGGCTGCTTGAGCCAACTCCATAGC
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                                                                                       C12R1:19),
(C12P21/02,C12R1:19),(C12P21/02,C12R1:91);
Strandedness. Double;
topology: Linear;
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Pred. No. 3.3e-96;
0; Mismatches 1
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                                                                                                                                             hypothetical: No;
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Bauer, S.Christopher, Abrams, M.Allen, Braford-Goldberg, S.Ruth,
Gaparon, M.Helena, Easton, A.Michael, Klein, B.Kure, McKearn, J.P.
Olins, P.O., Paik, K. and Thomas, J.W.
Co-administration of interleukin-3 mutant polypeptides with CS
for multi-lineage hematopoietic cell production
Patent: US 6093395-A 57 25-JUL-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
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          CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGGCTTCCTCCACAGGGCAGGACCACA
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Pred. No. 5.8e-96;
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Forstrom,J.W., Lofton-Day,C.E. and Lok,S.
Purified thrombopoietin and method of making
Patent: US 5986049-A 3 16-NOV-1999; 522 522 PAT ; 5 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCCTCTGCGTCAGG CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGG Score 518.8; DB 6 Pred, No. 5.8e-96; 0; Mismatches 228 AR087133 1062 bp DNA Sequence 3 from patent US 5986049. AR087133

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Unclassified.

1 (bases 1 to 1062)
Foster,D.C., Heipel,M.D. and Holly,R.D.
Methods for producing thrombopoletin polypeptides using a mammalian tissue plasminogen activator secretory peptide
Patent: US 5641655-A 3 24-UN-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1062)
                                                                                                                                                                                                                                                                                                                                                                                         61 TCCAGCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAAACTGCTTCGTGACTCC 120
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Pred. No. 5.8e-96;
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IS 5641655.
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3 from patent
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L36052
                                         GI:2471980
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Best Local Similarity 99.6'
Matches 520; Conservative
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            Sequence 149760
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GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG 480
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                                                                                                                      07-SEP-2000
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Holly, R.D., Lok, S., Foster, D.C., Hagen, F.S., Kaushansky, K., Kuijper, J.L., Lofton-Day, C.E. and Oort, P.J.
Methods for stimulating granulocyte/macrophage lineage using
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Pred. No. 5.8e-96;
0; Mismatches 2;
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375 c 236 g
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US
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Sequence 18 from patent
AR087571
                                                                                                                                                                                                                                                                              thrombopoietin
Patent: US 5989537-A 18
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source BASE COUNT ORIGIN

JOURNAL

TITLE

FEATURES

LOCUS

RESULT AR087571

ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS Length 1062; Indels

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1086)
                                                                                                                                                                                                                                                                A61K38/00, A01N1/02, C07K14/52//C12N15/09, C12P21/02, (C12P21/02,
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                                                                                                                               COMPOSITION CONTAINING THROMBOPOIETIN PROTEIN AND USED FOR STIMULATING RECOVERY OF HEMOSTATIC THROMBUS-FORMING ABILLITY PATENT: JP 1998212243-A 3 11-AUG-1998; KIRIN BREWERY CO LTD
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Location/Qualifiers
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99.6%; Pred. No. 5.8e-96;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type='Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product='signal .1086
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 386 c 243 g 22
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31-JAN-1997 JP 1997019549
KURODA KENJI
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                                                                                                                                                                                                                                                                                         strandedness: Double;
topology: Linear;
hypothetical: No;
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JP 1998212243-A/3
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                 GI:5711352
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                 E16669.1 GI:57113
JP 1998212243-A/3
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GPTCLSSLLGQLSGQVRLLLGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGKV
REMLVGGSTLVKRAPPTAVPSRTSLVLTLNBLPNRTSGLLETNFTASARTTGSGL
IKWQQGFRAX IPGLAVQTSRCLDQIPGYLNR IHELLNGTRGLFPGFSRRTLGAPDISS
GTSDTGSLPPNLQPGXSPSPTHPPTGQYTLFPLPPTLPTPVVQLHPLLDPDFSAPTFT
TSPLLNTSYTHSQNLSQEG"
                                                                                                                                                                                                     /product-"thrombopoietin"
/protein_id="AAG37566.1"
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/translation-"MELTELLIVVMLLLTARLTLSSPAPPACDLRVLSKLLRDSHVLH
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Foster, D.C., Sprecher, C.A., Grant, F.J., Kramer, J.M., Kuijper, J.L., McDlly, R.D., Whitemore, T.E., Heipel, M.D., Bell, L.A.N., Ching, A.F., McGrane, V., Hatt, C., O'Hara, P.J. and Lok, S.
Human thrombopoietin: gene structure, CDNA sequence, expression, and chromosomal localization
Proc. Natl. Acad. Sci. U.S.A. 91 (26), 13023-13027 (1994)
95108091
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Pred. No. 5.8e-96;
); Mismatches 2; Indels 0;
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I (bases 1 to 1267)

RS Miyazaki, H., Kato, H., Ogami, K., Iwamatsu, A., Akahori, H., Kuroki, R., Shimizu, T. and Muto, T.

RROTEIN HAYING TPO ACTIVITY

AL PROTEIN HAYING TPO ACTIVITY

AL PROTEIN HAYING TPO ACTIVITY

AL HOMO sapiens (human)

PN JP 1996277296-A, Z 22-OCT-1996;

KIRIN BREWERY CO LTD

OS Homo sapiens (human)

PN 1996277296-A, Z 22-OCT-1994 JP 94P 167328, PR

17-AGC-1994 JP 94P 227159, 17-AGC-1994 JP 94P 167328, PR

17-AGC-1994 JP 94P 155126, 15-JUN-1994 JP 94P 193169, PR

O1-JUN-1994 JP 94P 304167, 01-DEC-1994 JP 94P 298669, PR

O1-JUN-1994 JP 94P 341200

PI MIYAZAKI HIROSHI, KATO HISASHI, OGAMI KINYA, IWAMATSU AKIHIKO, PI AKAHORI HIRONORI, KUROKI RYOTA, SHIMIZU TOSHIYUKI, PI MUTO

TAKANORI

PC COTK44/52, COTH21/04, C12N15/09, C12P21/02/A61K38/00, (C12P21/02, PC C12R:19);

CC strandedness: Double;

CC strandedness: Double;

CC strandedness: Double;

CC copology: Linear;

FT Source Correction (Qualifiers

FT Source Correction (Promopopoietin)

FT Sig-peptide Series

FT Sig-peptide Correction (Promopopoietin)

FT Sig-peptide Correction (Promopopoietin)

FT Sig-peptide Correction (Promopopoietin)
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Pred. No. 5.6e-96;
0; Mismatches 2; Indels
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25. .1086
/product='thrombopoietin'
peptide 25. .87.
Location/Qualifiers
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/db_xref="taxon:9606"
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E12182.1 GI:3251016
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1267)
Miyazaki,H., Kato,H., Ogami,K., Iwamatsu,A., Akahori,H., Kuroki,R., Shimizu,T. and Muto,T.

PROTEIN HAVING TPO ACTIVITY
PROTEIN 17 1996291196-A 1 05-NOV-1996;
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PN JP 1965291196-A/1
PD 05-NOV-1996
PF 14-FEB-1995 JP 1995355052
PR 14-FEB-1994 JP 94P 39090, 25-MAR-1994 JP 94P 79842, PR 14-PEB-1994 JP 94P 155126, 15-JUN-1994 JP 94P 197128, PR 17-AUG-1994 JP 94P 197169, PR 17-AUG-1994 JP 94P 304167, 01-DEC-1994 JP 94P 197169, PR 2B-DEC-1994 JP 94P 341200
PI MIYAZAKI HIROSHI, KATO HISASHI, OGAMI KINYA, IWAMATSU AKI TAKANORI HIRONORI, KUROKI RYOTA, SHIMIZU TOSHIYUKI, PI MTAKANORI
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298669, PR
145 CATGTCCTTCACAGCGAGACTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC
                                                                               205 CTGCTGCTGCTGTGGAGCTTTAGCTTGGGAGAATGGAAAACCAGATGGAGGAGACCAAG
                                                           CTGCTGCCTGCTGTGGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG
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25. .87
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25. .1086
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Human cDNA encoding thrombopoietin.
E12214 GI:3251048
JP 1996291196-A/1.
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88. .1083
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strandedness: Double;
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                                                              Score 518.8; DB 6;
Pred. No. 5.6e-96;
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Pred: No. 5.5e-96;
); Mismatches 2;
                           271
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Elliott, S.G.
Mpl ligand analogs
Patent: US 5756083-A 1 26-MAY-1998,
1. .1267
/organism="Homo sapiens"
/db_xref="taxon:9606"
a 436 c 279 g 27
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Sequence 1 from patent US 5756083.
AR008878 GI:3967683
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454 c 293 q
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Best Local Similarity 99.6%;
Matches 520; Conservative
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1 (bases 1 to 1342)
BartLey, T.D., Bogenberger, J.M., Bosselman, R.A., Hunt, P.,
Kinstler, O.B. and Samal, B.B.
Mono-pegylated proteins that stimulate megakaryocyte growth and
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36 ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG
                                                                                                                                             CTGCTGCCTGCTGTGGACTTTAGCTTGGGAAATGGAAAACCCAGATGGAGGAGACCAAAG
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Pred. No. 5.5e-96;
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Patent: US 5795569-A 24 18-AUG-1998;
Location/Qualifiers
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454 c 293 a
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Sequence 24 from patent US
AR023468
AR023468.1 GI:3976762
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                                                                                                                     GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG
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                                                    CTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGGAGCAAG
                                                                                                                                                                                               CAACTGGGACCCACTTGCCTCTATCCTTGGGGCCAGCTTTCTGGACAGGTCCGTCTC
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1. .1342
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454 c 293 g
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Sequence 1 from patent US 50
AR087573
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Elliott,S.G.
Mpl ligand analogs
Patent: US 5989538-A 1
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CAACTGGGACCCACTTGCCTCTCATCCCTCTGGGCAGCTTTCTGGACAGGTCTCTC
                                                                                                                   GCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGAGTGATGGCAGCACGGGGA
                            336 CAACTGGGACCCACTTGCCTCTCATCCCTCTGGGGCAGCTTTCTGGACAGGTCCGTCTC
                                                           CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGGCTTCCTCCACAGGGCAGGACCACA
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Pred. No. 5.5e-96;
0; Mismatches 2;
                                                                                                                                                                                                 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGG
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Patent: US 5696250-A 1 09-DEC-1997;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                            DNA
US 5696250
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454 c 293 g
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1 from patent
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Elliott, S.G.
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Matches 520; Conservative
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481 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGG 522
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Submitted (08-JUL-1994) to the DDBJ/EMBL/GenBank databases. Kinya
Submitted (08-JUL-1994) to the DDBJ/EMBL/GenBank databases. Kinya
Ogami, KIRIN Brewery Co., Ltd., Pharmaceutical Research Laboratory;
2-2 Soujamachi 1 chome, Macbashi, Gunma 371, Japan
(Tel:0272-54-8618, Fax:0272-52-2307)
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SRLSQCPEVHPLPTPVLLPAVDFSLGEWKTQMEETKAQDILGAVTLLLEGVWAARGQL
GYPCLSSLLGQLSGQVRLLLGALQSLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGKV
RFPMLVGGSTLCVRRAPPTAVPSRTSLVTLNELPNTTSGLLETVFTASRTTGSGL
LKWQQGFRAK LPGLLAGYTSKSLDQIPQYLNRTHELNVTRGLFPGSARTTGSGL
LKWQQGFRAK LPGLLAGYTSKSLDQIPQYLNRTHELNVTRGLFPGPSRRTLGAPDISS
GTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPPPTPTVVQLHPLLPDFSAPTPTP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1691)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rato, T., Ogami, K., Shimada, Y., Iwamatsu, A., Sohma, Y., Akahori, H.,
Horie, K., Kokubo, A., Kudo, Y., Macda, E., Kobayashi, K., Ohashi, H.,
Dawa, T., Inoue, H., Rawamura, K. and Miyazaki, H.
Purification and characterization of thrombopoietin
J. Biochem. 118 (1), 229-236 (1995)
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                                                                                                                                   03-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Erratum:{[published erratum appears in J Biochem (Tokyo) 1996
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Homo sapiens mRNA for thrombopoietin, complete cds.
D32047
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481 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGG 522
                     516 CGTTTCCTGATGCTTGTAGGAGGTCCACCCTCTGCGTCAGG 557
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Pred. No. 5.1e-96;
0; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="thrombopoietin"
/protein_id="BAA21930.1"
/db_xref="GI:2351118"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="liver"
102 .164
                                                                                                                                                                                                                             Homo sapiens liver cDNA to mRNA
Homo sapiens
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ACCESSION
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ORIGIN
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                                                                                                                                      CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA
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Search completed: April 5, 2002, 10:29:40 Job time: 4773 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Fusion peptide #3	Fusion peptide #2	Fusion peptide #1	Thrombopoietin cod	Human thrombopoiet	Sequence encoding	Human thrombopoiet				
SUMMARIES	AAT41788	AAT41787	AAT41786	AAQ99552	AAT03941	AAT04050	AAT34852	AAT37383	AAT32591	AAT85555	AAV21696
DB	17	17	17	16	16	16	17	17	17	18	19
% Query Match Length DB	1095	1083	1047	861	1062	1062	1062	1062	1062	1062	1062
% Query Match	100.0	94.1	90.2	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4
Score	1095	1030.2	987.4	518.8	518.8	518.8	518.8	518.8	518.8	518.8	518.8
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	Native human mpl l Human MGDF-1/2 cDN Thrombopoietin cod	Human wild type th Human thrombopoiet	hML cDNA. Homo sa	Human thrombopoiet	Human truncated mp	Thrombopoietin cod	Plasmid pASN6 enco	Plasmid pASN145 en	Plasmid pAS28 enco	Human megakaryocyt	Nucleotide sequenc	Human mpl ligand e	Flt3L/IgG2b/G-CSF	Flt3L/IgG2b/G-CSF	Flt3L/GS/G-CSF clo	Flt3L/GS/G-CSF clo	Human flt3 ligand	Nucleic acid segue	G-CSF-Flt-3 ligand	Nucleic acid seque	G-CSF gene isolate	Plasmid pBRV2 inse	Sequence encoding	Plasmid pBRV2 inse	Sequence encoding	Plasmid pP12 contg	pMON13056 DNA enco
AAA51991 AAT47958 AAQ99704	AAT36657 AAT10025 AA099554	AAZ40191 AAA47793	AAQ94107	AAT64318	AAX32813															AAV70391	AAN80947	AAN70223	AAN71320	AAN60937	AAN81478	AAN91086	AAQ97174
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13	15 16	118	20	21	23	24	52	56	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT

Fusion protein; human granulocyte colony stimulating factor; hG-CSF; thrombopoietin; TPO; spacer peptide; blood platelet production; leukocyte production; anaemia; ds. Terasaki Y; Fusion peptide #3 having G-CSF and TPO activity. Anazawa H, Konishi N, Shiotsu Y, Tamaoki T, Uchida K, Yamasaki M, Yamashita K, Yokoi H; Location/Qualifiers AAT41788 standard; DNA; 1095 BP. (KYOW) KYOWA HAKKO KOGYO KK. 96WO-JP01157. 95JP-0102625. (first entry) 1..63 /*tag= a 64..1095 /*tag= b 26-APR-1996; WO9634016-A1 26-APR-1995; Homo sapiens 01-JUL-1997 sig_peptide 31-OCT-1996. mat_peptide AAT41788; AAT41788

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Claim 3; Page 49-51; 71pp; Japanese
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                                       Fusion peptide having G-CSF and with thrombopoietin activity - optionally chemically modified with a poly:alkylene glycol, used for
                                                                                                                                                                                                                                                                1 ATGGAGCTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG 60
                                                                                               The sequences given in AAT41786-88 encode fusion proteins which are composed of a peptide having human granulocyte colony stimulating factor (NG-CSF) activity fused with a peptide having thrombopoletin (TPO) activity, opt. via a spacer peptide. Peptides derived from these by deletion, insertion or substitution of one or more amino acid residues are included within the scope of the invention. The fusion peptides stimulate blood platelet and leukocyte production and are useful in the treatment of anaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1095;
                                                                                                                                                                                           Sequence 1095 BP; 194 A; 362 C; 311 G; 228 T; 0 other;
                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                      100.0%; Score 1095; DB 17;
100.0%; Pred. No. 1e-247;
tive 0; Mismatches 0;
                                                                               Claim 3; Page 52-54; 71pp; Japanese.
                                                                                                                                                                                                                                             Conservative
                                                           treatment of anaemia
         WPI; 1996-497573/49.
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Best Local Similarity
Matches 1095; Conserv
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CAGCTGCCAGGCTGCTTGAGCCAACTCCATAGCGGCCTTTTCCTCTACCAGGGGCTCCTG
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Yamashita K,
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                                                                                                                                                        Length 1083;
                                                                                                                                                                              12;
                                                                                                                                                                              13; Indels
                                                                                                                   Sequence 1083 BP; 197 A; 355 C; 305 G; 226 T; 0 other;
                                                                                                                                                     17;
                                                                                                                                                     Score 1030.2; DB 17
Pred. No. 1.6e-232;
); Mismatches 13;
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97.7%;
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Matches 1070; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 hG-CSF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             composed of a peptide having human granulocyte colony stimulating factor (hG-CSF) activity fused with a peptide having thrombopoietin (TPO) activity, opt. via a spacer peptide. Peptides derived from these by deletion, insertion or substitution of one or more amino acid residues are included within the scope of the invention. The fusion peptides stimulate blood platelet and leukocyte production and are useful in the treatment of anaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences given in AAT41786-88 encode fusion proteins which are
                                                          CAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGAC
            CTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGCGCCGGGCAGGA
                                                                                                                                             GGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTCCTGGAGGTGTCGTACCGCGTTCTACGC
                                               GTCGCCGACTTTGCCACCACCATCTGGCAGCAGAAGAAGAACTGGGAATGGCCCCTGCC
                                                                                                                                                                                                                                                                                                                                                                                Fusion protein; human granulocyte colony stimulating factor; hG
thrombopoietin; TPO; spacer peptide; blood platelet production;
leukocyte production; anaemia; ds.
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                                                                                                                                                                                                                                                                                                                                                         Fusion peptide #1 having G-CSF and TPO activity
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Yamashita K,
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P-PSDB; AAW00377.
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Thrombopoietin; TPO; humoral factor; platelet; antibody; therapy; AIDS; thrombocytopenia; hypoplastic anaemia; thrombotic thombocytopenia; disseminated intravascular coagulation syndrome; ds.
                                          GGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTCCTGGAGGTGTCGTACCGCGTTCTACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietin polypeptide which specifically stimulates increases platelet production - useful in treatment of thrombocytopenia, also related DNA and vectors
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                                                                                                                                                     AAQ99552 standard; cDNA to mRNA; 861
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
25..783
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Ohgami K, Shimizu T;
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94JP-0193916.
94US-0320300.
94JP-0304167.
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94JP-0341200.
95US-0381478.
94JP-0227159.
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P-PSDB; AAR81378.
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01-JUN-1994;
15-JUN-1994;
20-JUL-1994;
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22-DEC-1994;
28-DEC-1994;
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18-AUG-1994;
11-OCT-1994;
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25-MAR-1994;
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Muto T,
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                                                                 48;
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           0 other;
                                          DB 17;
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Pred. No. 1.7e-222;
0; Mismatches 1;
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ilarity 95.5%;
Conservative
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Matches 1046; Conserv
          Sequence 1047
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      This sequence represents the coding sequence for a thrombopoietin (TPO) protein. TPO is a humoral factor capable of promoting platelet production. The encoded protein can be purified by using a gel affinity column where Mpl has been coupled to a reain. AAAQ99551 and AAQ99553 also encode TPO proteins. The DNA sequences are inserted into vectors which are used to transform prokaryotic and eukaryotic host cells. Using the proteins encoded by these sequences, and derivatives of them, antibodies specifically immunoreactive with a TPO protein can be created. The antibodies. DNA sequences and vectors are used to isolate the protein sequences. The TPO proteins can then be used in the treatment of platelet disorders. These include thrombocytopenia, hypoplastic anamemia, ADDS, disseminated intravascular coagulation syndrome and
                                                                                                                                                                                                                                                                                  CICCITGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
                                                                                                                                                                                                                                                         CAACTGGGACCCACTTGCCTCTCATCCCTCTGGGGCAGCTTTCTGGACAGGTCCGTCTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG 480
                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG
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0
                                                                                                                                                                     Score 518.8; DB 16; Length 861;
Pred. No. 1.3e-112;
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thrombopoietin; erythropoiesis stimulator; treatment;
                                                                                                                                         Sequence 861 BP; 243 A; 257 C; 197 G; 164 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                     47.48;
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                                                                                                                     thrombotic thrombocytopenia.
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                                                                                                                                                                                        Conservative
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Best Local Similarity
Matches 520; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stimulation of erythropoiesis using thrombopoietin and opt. erythropoietin - for the treatment of thrombocytopenia and anaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erythropoiesis to produce an increase in proliferation or differentiation of erythroid cells or to increase reticulocyte counts at least 2-fold over baseline reticulocyte counts and, optionally, platelet levels to at least 20000/cu mm. The protein can be used in a composition, optionally with erythropoietin, for use in the treatment of thrombocytopenia and anaemia, such as that caused by destruction of haematopoietic cells in bone marrow, in the treatment of cancer with chemotherapy and radiation, and in pathological conditions such as myelodysplasia, AIDS, aplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence encodes human thrombopoietin, which stimulates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1062 BP; 223 A; 375 C; 236 G; 228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anaemia, autoimmune disease or inflammatory disease.
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0; Mismatches 2;
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Location/Qualifiers
1..1062
/*tag= a
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94US-0196025.
94US-0203197.
94US-0215203.
94US-025491.
94US-0335566.
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                                                                                                                                                                                                                                                                           New low mol. wt. forms of thrombopoietin and related DNA - vectors and transformed cells, useful for stimulating platelet prodn. esp. for treatment of thrombocytopenia
                                                                                                                                                                                                                                                                                                                                 GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG
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P-PSDB; AAR98947.
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SG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                    GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG
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                                                                                                                                                                                                                                                                                                                              lesis; protein; bone marrow; stem cells; precursor;
therapy; ds.
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                                                                                                                         CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= Haematopoietic protein.
                                                                                                                                      1.4e-112;
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                                                                                                                                                                                                                                                                                                     Sequence encoding haematopoietic protein.
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94US-0196025.
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94US-0215203.
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99.68;
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hes 520; Conservative
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Kuijper JL, Lofton-day
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P-PSDB; AAR79906.
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25-FEB-1994;
21-MAR-1994;
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AAT04050;

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RESULT

AAT04050

522 522 A cDNA clone (AAT34852) codes for human thrombopoietin (AAR98947), a

1 ATGGAGCTGAACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG 60

Query Match

Best Loca Matches

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Forstrom JW,
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                                                                                                                                                                                                                                                                                                                          CAACTGGGACCCACTTGCCTCTCATCCCTCGGGGCAGCTTTCTGGACAGGTCCGTCTC 360
                                                                                                                                                                                                                                                                                                                                                               TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
                                                                                                                                                                                                                tecageceggetectectgettgtgacetecgagtecteagtaaactgettegtgactec 120
                                                                                                                                                                                                                                     CATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC 180
                                                                                                                                                                                                                                                       catgiccticacagcagactgagccagigcccagaggitcacccittigcciacacctgic 180
                                                                                                                                                                                                                                                                                                                                                                                           CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG 480
protein that stimulates megakaryopoiesis and thrombocytopoiesis. The cDNA can be incorporated into an expression vector and utilised in the prodn. of low mol.wt. bioactive human thrombopoietin in thrombopoietin (partic. yeast or mammalian) host cells. The recombinant thrombopoietin has an N-terminus at Ser-22 and a C-terminus between Arg-185 and Asn-192 (esp. Arg-198 or Phe-207), and is useful for increasing platelet prodn. in the treatment of thrombocytopenia or for increasing proliferation of cells in bone marrow.
                                                                                                                                      Gaps
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                                                                                                                                                        ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG 60
                                                                                                                                                                                                                                                                                    TPO; aplastic anaemia; congenital cytopaenia; syndrome; megakaryocytopoiesis; thrombocytopoiesis; transgenic animal; ds.
                                                                                                                                                                 CTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGAGACCAAG
                                                                                                                                                                                                                                             DB 17; Length 1062;
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                                                                                                                                     Indels
                                                                                      Sequence 1062 BP; 223 A; 375 C; 236 G; 228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cgtttcctgatgcttgtaggagggtccaccctctgcgtcagg 522
                                                                                                                 Score 518.8; DB 17
Pred. No. 1.4e-112;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGG
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                                                                                                                   47.48;
99.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human thrombopoietin cDNA.
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/*tag= a
67..1059
                                                                                                                  Query Match 47.4
Best Local Similarity 99.6
Matches 520; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT37383 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haematopoiesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myelodisplatic
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A cDNA clone (AAT37383) codes for human thrombopoietin (TPO) (AAW03512)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAACTGGGACCCACTTGCCTCTCATCCCTGGGGCAGCTTTCTGGACAGGTCCGTCTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CATGTCCTTCACAGCAGAGTGAGCCAGGGGCTCAGAGGTTCACCCTTTGCCTACACCTGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CICCITGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
                                                                                                                                                                                                                                                                                                                                        It was isolated by PCR from human liver and kidney cDNA templates using primers (see also AAT37385-88) derived from exon sequences of a human genomic TPO clone (see also AAT37384) and from the conserved 5' untranslated sequence of mouse TPO cDNA (AAT37382). The cDNA can be used to produce recombinant mature TPO in transformed host cells. Purified, homogeneous TPO is obtd. that is suitable for therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                        wt. degradation prods.
congenital cytopaenia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 518.8; DB 17;
Pred. No. 1.4e-112;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New pure thrombopoietin free of low mol. v
useful for treatment of aplastic anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1062 BP; 223 A; 375 C; 236 G;
                                                                                                                                                                                                                                                                                   Example 2; Page 63-65; 92pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.48;
                                                                                                                    Lofton-Day CE,
95WO-US16626
                                      94US-0366859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                520; Conservative
                                                                              (ZYMO ) ZYMOGENETICS
                                                                                                                                                             WPI; 1996-333942/33.
P-PSDB; AAW03512.
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In a claimed method, thrombopoietin (TPO) (especially human TPO) is administered to a donor to stimulate proliferation of myeloid cells. Bone marrow or peripheral blood stem cells are collected from the donor and administered to the recipient. The method is used for preparing cells for (bone marrow) transplantation and for stimulating
                                                                                      GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG 480
                                                                                                                                                                                                                                                                                              Increasing haematopoietic cells in patient - by admin. of stem cells from donor previously treated with thrombopoietin, used in patients who have received chemotherapy or radiation for cancer
CAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTC
                                                                                                                                               CTCCTTGGGGCCCCTGCAGAGCCTCCTTGGAACCCAGGCTTCCTCCACAGGGCAGGACCACA
                                                                                                                                                                                                                                       ctccttggggccctgcagagcctccttggaacccagcttcctccacagggcaggaccaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO; cancer; myeloid cell proliferation; expansion; bone marrow; peripheral blood stem cell; chemotherapy; radiation therapy; breast cancer; leukaemia; lymphoma; multiple myeloma; ds.
                                                                                                                                                                                                                                                                                                                                               522
                                                                                                                                                                                                                                                                                                                                                                    481 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 17-19; 32pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-108626/10.
P-PSDB; AAW26841.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA construct encoding native mammalian tissue plasminogen activator secretory peptide and thrombopoietin polypeptide - used to produce thrombopoietin polypeptide(s) on a large scale and in cost effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin; TPO; tissue plasminogen activator; cytokine; protein secretion; signal peptide; thrombocytopenia; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.4%; Score 518.8; DB 17; Length 1062; 99.6%; Pred. No. 1.4e-112; ive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1062 BP; 223 A; 375 C; 236 G; 228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 41-43; 56pp; English.
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1..63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holly RD;
                                                                       AAT32591 standard; cDNA; 1062 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of thrombocytopenia.
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64..1059
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                                                                                                                                               (first entry)
                                                                                                                                                                                 Human thrombopoietin cDNA
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Matches 520; Conserv
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                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-NOV-1994;
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AAT32591
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platelet or erythrocyte recovery in a patient receiving chemotherapy or radiation therapy for e.g. breast cancer, leukaemia, lymphoma or multiple myeloma. Treating the donor with TPO accelerates restoration of erythrocyte and thrombocyte levels in the patient after transplant. This restoration may be further improved by administering TPO to the recipient after transplant. The present sequence encodes human TPO.
                                                                                                                                                                                                                                                                                                                                                                                                                       480
                                                                                                                                                                                                                                                                                                            CATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCGAGCTTCCTCCACAGGGCAGGACCACA 420
                                                                                                                                                                                                                                                      TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       getcacaaggateceaatgecatetteetgagetteeaacacetgeteegaggaaaggtg 480
                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                   CTGCTGCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG
                                                                                                                                         Score 518.8; DB 18; Length 1062;
Pred. No. 1.4e-112;
); Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                   Sequence 1062 BP; 223 A; 375 C; 236 G; 228 T; 0 other;
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                                                                                                                                           47.4%;
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                                                                                                                                                        Similarity
                                                                                                                                         Query Match
Best Local Simi
Matches 520;
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This cDNA encodes a thrombopoietin (TPO) polypeptide. This can be used in the construction of a new expression vector replicable in a cuaryotic host cell encoding TPO polypeptides. The vector comprises a transcription promoter, a first DNA segment encoding a secretory leader, a second segment encoding a TPO polypeptide and a transcription a second segment encoding a TPO polypeptide and a transcription terminator which are all operably linked. The second TPO segment consists of C-X-B, where C is a human TPO cytokine domain, X is a peptide bond or a linker consisting of one or two amino acid residues, such that X along in combination with C or B does not provide a dibasic maino acid pair and B is a polypeptide that can be selected from AAM53125 to AAM53126. The secretory leader is a S. cerevisiae alpha-factor secretory leader. A cultured yeast cell containing such an expression vector can be used to produce the TPO polypeptide. The TPO polypeptide can be used to increase for increasing platelet number in a mammal. It can be used to increase them charactery or congenital cytopenias. It can also be used to treat the charactery or congenital cytopenias. It can also be used to treat the characteries of the second production of sord disorders, such as leukaemia and lymphoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19;
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Pred. No. 1.4e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or metastatic cancers involving bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                              Thrombopoietin protein expression vector
                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Pages 29-32; 56pp; English.
                                                                                                                                                                                                                                         Irani M, Morrison-nelson GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.48;
99.68;
                                                                                                                                    97WO-US13543.
                                                                                                                                                                                                                                                                                                                                               platelet number in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 99.6
Matches 520; Conservative
                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                          WPI; 1998-159541/14.
                                                                                                                                                                                                                                                                                          P-PSDB; AAW53124
                                                               WO9806849-A1
                                                                                                                                    30-JUL-1997;
                                                                                                                                                                      13-AUG-1996;
                                                                                                   19-FEB-1998
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                                                                                             Local
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Erthyropoiesis may be stimulated in anaemic mammals by administration of thrombopoietin (TPO), and optionally erythropoietin (EPO). The anaemic mammal to be treated will have shown a haematocrit level less than 39 percent of total blood volume, a reticulocyte count of less than 0.8 percent and may have been treated with radiation or chemotherapy. Timproved red blood cell level is due to an increase in red blood cell proteins may be used therapeutically to increase proliferation of proteins may be used therapeutically to increase proliferation of proteins may be used therapeutically to increase proliferation of cytopenia or anaemia, especially associated with bone marrow failure, disorders associated with low red blood cell production, particularly when accompanied by thrombocytopenia and for increasing the level of
301 caactgggacccacttgcctctcatcctcctggggcagctttctggacaggtccgtctc 360
                                                                               or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stimulating erythropoiesis e.g. for treating anemias or cytopenia, or for ex vivo expansion of marrow or peripheral blood progenitor cell, comprises administering thrombopoietin alone or in combination with
                                                                                                                                                                                                                                                                                        Thrombopoietin; TPO; erythropoietin; EPO; erthyropoiesis; stimulate; anaemia; radiation; chemotherapy; red blood cell production; haematopoietic cell; cytopenia; ex vivo expansion; anti-anaemic;
                      CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA
                                               ctccttgggggccttggaggcctccttggaacccagcttcctccacagggcaggaccaca
                                                                    GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG
                                                                                                                             CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGG
                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Column 19-22; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                 AAA51991 standard; cDNA; 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0288417
94US-0335566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0999927
                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                    Human thrombopoietin cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UNIW ) UNIV WASHINGTON. (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-557618/51.
P-PSDB; AAY97136.
                                                                                                                                                                                                                                                                                                                            Lmmunomodulator; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erythropoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (aushansky K;
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                              04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                 US6099830-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-AUG-2000
                                                                                                                                                                                                                      AAA51991;
                        361
                                            361
                                                                   421
                                                                                                                 481
                                                                                                                                       481
                                                                                                                                                                          RESULT 1
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erythrocytes and erythrocyte precursor cells. TPO and EPO may ex vivo expansion of marrow or peripheral blood progenitor
                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                            240
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                                                                                                                                                                                                                        CTGCTGCTGCTGTGGACTTTAGCTTCGGAGAATGGAAAACCCAGATGGAGGAGACCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG
                                                                                                                                                                                                                                                                                                                                                     CATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ctgctgcctgctgtggactttagcttgggagaatggaaaacccagatggaggagaccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAACTGGGACCCACTTGCCTCTCATCCCTCGGGGCAGCTTTCTGGACAGGTCCGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG
                                                                                                                              DB 21; Length 1062;
                                                                                                                                                                   ;
0
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                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
88..1083
/*tag= c
/note= "mature protein residues.1-332"
                                                                        Sequence 1062 BP; 223 A; 375 C; 236 G; 228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                            47.4%; Score 518.8; DB 21
99.6%; Pred. No. 1.4e-112;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human thrombopoietin (1-332) coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "immature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT47958 standard; cDNA to mRNA; 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
25..1086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                   520; Conservative
                                                                                                                                                 Similarity
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Mpl ligand; mammalian megakaryocyte growth promoting factor;
                                                                        platelet producing factor; ss
                                            Human MGDF-1 and MGDF-2.
                                                                                                                                                                                                                                                                                         WPI; 1995-338287/44
                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                       Kinstler OB,
                                                                                        Homo sapiens
                           01-FEB-1996
                                                                                                                                                                                30-MAR-1995;
                                                                                                                                                                                                30-NOV-1994;
                                                                                                                                                                                                         31-MAR-1994;
                                                                                                                                                                                                                           12-OCT-1994;
                                                                                                                                                               04-OCT-1995
                                                                                                                                             EP675201-A.
          AAQ99704;
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                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                   CTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAACTGGGACCCACTTGCCTCTCATCCCTCGGGGCAGCTTTCTGGACAGGTCCGTCTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stable thrombopoietin (TPO) compsns. containing TPO and an additive, pref. human serum albumin and/or gelatine, etc., are claimed. The compsns. do not lose TPO activity on storage in a container as the compsn. has reduced adsorption onto the container walls. The present sequence encodes recombinant immature human TPO (1-332).
                                                                                                                                                                                                                                                                                                                                                                     CATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                             ctgctgcctgctgtggactttagcttgggagaaatggaaaacccagatggaggagaccaag 264
                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catgiccticacagcagactgagccagigcccagaggitcaccctitgcciacaccigic 204
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                 ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTG 60
                                                                                                                                                                                                                                                                                                          Stable thrombopoietin compositions contains TPO and an additive does not lose thrombopoietin activity on storage in a container
                                                                                                                                                                                                                                                             Score 518.8; DB 17; Length 1086;
Pred. No. 1.4e-112;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                   Sequence 1086 BP; 229 A; 386 C; 243 G; 228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGG 522
                                                                                                                                                             Example 1; Page 26-28; 38pp; Japanese.
                                                                                                                                                                                                                                                              47.48;
99.68;
                                   96WO-JP00635.
                                                    95JP-0056248
                                                                                                                                                                                                                                                                                Conservative
                                                                      (KIRI ) KIRIN BREWERY KK
                                                                                                       WPI; 1996-433541/43.
                                                                                                                                                                                                                                                                       Similarity
                                                                                                                 P-PSDB; AAW09314
WO9628181-A1
                                  14-MAR-1996;
                                                    15-MAR-1995;
                                                                                                                                                                                                                                                            Query Match
Best Local Simi
Matches 520;
                19-SEP-1996
                                                                                        Otsuki N;
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94US-0347780. 94US-0221768. 94US-0252628. 94US-0321488.

95EP-0104711.

Location/Qualifiers 36..1097 /*tag= a

(first entry)

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                                                                   New human megakaryocyte growth and development factor - used to increase the number of megakaryocytes or platelets in patients, e.g. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGDE-2) is active supports this hypothesis. Various active molecules that may result from truncations of the sequence set forth as MGDE-1 (AAR80824, aAR80825, aAR80825, AAR80825 aAR80826 as the signal peptide. The preferred truncation variants of MGDE-1 are any of those that have C-terminal truncations from AA 173-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mpl ligand is synonymous with MGDF. Mpl ligands are mammalian megakaryocyte growth promoting and/or platelet producing factors. MGDF-1 is a truncated portion of MGDF-1. It is hypothesised that human MGDF is expressed in vivo as a substantially inactive or less active precursor polypeptide that contains variable C-terminal AAs. Upon cleavage of the C-terminal AAs (as well as the signal peptide), the processed form(s) of the molecule retain activity or become more active. It is believed that MGDF-1 may require processing in order to exhibit its activity. The fact that a truncated form MGDF-1 (i.e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
P-PSDB; AAR80821, AAR80822, AAR80823, AAR80824, AAR80825, AAR80826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (along with cleavage of the signal peptide). The signal peptide
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Pred. No. 1.5e-112;
0; Mismatches 2;
                                                                                                                                                                                                                Claim 17; Fig 11; 98pp; English.
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Best Local Similarity 99.6%;
Matches 520; Conservative
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AAQ99704 standard; cDNA; 1342

RESULT 14

AAQ99704 ID AAO9

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Disclosure; Fig 1; 106pp; English
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Job time: 4956 sec
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                           CTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG
                                                      GCACAGGACATICTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGA
                                                                                CAACTGGGACCCACTTGCCTCTCATCCCTCGGGGCAGCTTTCTGGACAGGTCCGTCTC
                                                                                                                                    GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTG
                                                                                                                                                   gctcacaaggatcccaatgccatcttcctgagcttccaacacctgctccgaggaaaggtg
                                                                                                                                                                                                                                                                   Native human mpl ligand; altered glycosylation pattern; carbohydrate side chain; sialic acid content; thrombocytopaenia; megakaryocyte/platelet deficiency; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence with added, deleted useful in compsns. to treat
                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= Full_length_mpl_ligand
36..98
                                                                                                                                                                        CGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTACGG
                                                                                                                                                                                                                                                        Native human mpl ligand coding sequence
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36..1097
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This sequence encodes native human mpl ligand. The invention concerns analogues of mpl ligand which have altered glycosylation patterns. Alteration of glycosylation of mpl ligand can cause improved biological activity. The mutated proteins comprise a greater or lesser number of carbohydrate side chains and higher or lower sialic acid content than wild type mpl ligand. Compositions comprising the mpl ligand analogues of the invention may be used to treat diseases involving an existing or expected megakaryocyte/
                                                                                                                                                                                                                                                                                                                                                                                                         ATGGAGCTGACTGACTCCTCCTCGTGCTATCTTCTCTAACTGCAAGGCTAACGCTG
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llarity 99.6%; Pred. No. 1.5e-112;
Conservative 0; Mismatches 2;
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Best Local Similarity
Matches 520; Conserv
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UI-R-C2p-PII_84_E1 EM1_68_F0 602687225

zo70d02.s Tetraodon

Perfect score: Sequence:

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Scoring table:

Searched:

Database

Drosophil

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bb13b10.y xr35c05.x hx79f09.x fh07b05.x 602578852 Tetraodon x173e08.x

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Tetraodon

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Result Ş. 320.4 312.8 301.6 300.6 2099.6 227.8 135.2 106.2 86.4

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Best Local Similarity 99.4%;
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1 (bases 1 to 598)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            950 TGGCCCCTGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGC 1009
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Pred. No. 1.2e-61;
0; Mismatches 116; Indels
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BG548320.1 GI:13546985
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Best Local Similarity 77.1%;
Matches 390; Conservative
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AUTHORS
TITLE
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be http://image.lln.gov

Plate: LLCM1541 row: b column: 24

High quality sequence stop: 597.

Location/Qualifiers

1. 598

/Organism="Homo sapiens"
/Ab_Arref="taxon:9606"
/Ab_Arref="Arref="Taxon:9606"
/Ab_Arref="Taxon:9606"
/Ab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 5.2e-60;
0; Mismatches 2; Indels 0;
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Wells.K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="pooled"
//lab_host="publis"
//lab_host="publis"
//lab_host="publis"
//lab_host="publis"
Library made from pooled mRNA isolated from mammary
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
a 170 c 158 g 82 t
                                                                                                                                                                                                                                                                                     Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                   Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidee; Bovinee; Bos.
1 (bases 1 to 507)
Sonstegard, T.S., Capuco, A.V., Van Tassell, C.P., Ashwell, M.S. and
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                         USDA, ARS, Beltsville Agricultural Research Center Balg. 200 Rm 2A, Beltsville, MD 20705, USA Tel: 301 504 8416 Fax: 301 504 8414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: 134 row: J column: 17
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG
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84.1%;
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                                                                   L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-Temail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://nage.lln.gov
Plate: LLAMIJ338 row: g column: 19
High quality sequence stop: 808.
Location/Qualifiers
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NCI_CGAP_Lig"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: liver; Vector: pcWv-sPoRT6; Site_l: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 290 c 223 g 192 t l others
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                 1 (bases 1 to 900)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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172130 BARC 5BOV Bos taurus CDNA 5', mRNA sequence.
BE485194
BE485194.1 GI:9604727
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5137578"
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                                   Gaps
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Length 507;
                                   64; Indels
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Score 300.6; DB 10;
Pred. No. 2.7e-57;
                                   0; Mismatches
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358 CACCTCCTTCACAGCCGACTGAGTCTCCCGACGTCGACCCTTTGTCTATCCCTGTT 417
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/lab.host="DHIOB"
/lab.host="DHIOB"
/loce="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACGTGTG); Site_2: braIII (GACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTATGTG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACGTGTG, 3' site CACATGTG). XhoI should
be used to isolate the CDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCACA."

25 a 210 c 166 g 131 t 1 others
                                                                                                                                                                                             Mus musculus

Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammala; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 633)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Morris,M.,

Thelsing,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                A1314551 633 bp mRNA EST 17-DEC-1998 14862.0; Y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1923186 5' similar to qb::134169 Mus musculus thrombopoietin mRNA, complete cds (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:979418
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 300.6; DB 10; Length 633;
Pred. No. 2.8e-57;
0; Mismatches 60; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL"
/db_xref="Ftaxon:10090"
/clone="IMAGE:1923186"
/clone_lib="Sugano mouse liver mlia"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
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High quality sequence stop: 505.
Location/Qualifiers
1. 633
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AI314551.1 GI:4029818
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                                                                                                                                                                             house mouse.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (base; 1 to 609)

88 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Morre, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Materston, R.

The Washu-HHMI Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810

Email: mouseestwatson, wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vj03a07.rl Barstead mouse pooled organs MPLRB4 Mus musculus CDNA clone IMAGE:920628 5' similar to gb:L34169 Mus musculus thrombopoietin mRNA, complete cds (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royally-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:532844
                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1997
CAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTC
                                                                                                                                                                                                 /organism="Mus musculus"
/strain="rWB/N"
/db_xrsfe="taxon:10090"
/clone="IMAGE:220628"
/clone=lib="Barstead mouse pooled organs MPLRB4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 492.
Location/Qualifiers
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Matches
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AUTHORS
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COMMENT
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mans musculus
Rumania; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 878)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
Plate: LLAM9810 row: i column: 08
High quality sequence stop: 628.

Location/Qualifiers
                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF789308 878 bp mRNA EST 12-JAN-2001
602104729F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4222927
                                                                         TCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCC 120
                                                                                                                               CATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC 180
                                                                                                                                                                                           CTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG 240
                                                                                                                                                                                                                                                  CAACTGGGACCCACTTGCCTCTCATCCCTCGGGGCAGCTTTCTGGACAGGTCCGTCTC 360
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                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 609;
                              Indels
   DB 10;
                           69
Score 299.6; DB 1
Pred. No. 4.7e-57;
0; Mismatches 69
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/clone_lib="NCI_CGAP_Kid14"
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27.4%;
ilarity 81.6%;
Conservative
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BF789308
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             Similarity
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                           Matches 364;
Query Match
Best Local 8
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ORGANISM
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KEYWORDS
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ingle pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [ (bases 1 to 464) Smith, Freking, B.A., Roberts, A.J., Stone, R.T., Gasse, M.M., Freking, B.A., Roberts, A.J., Stone, R.T., Wary, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG 240
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                                                                                                                                                                                                                                                       Score 285.2; DB 11; Length 878;
Pred. No. 8.5e-54;
); Mismatches 58; Indels 0;
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200137 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BE754587.1 GI:10168579
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4369
                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                       26.0%;
llarity 84.7%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CICITGGGGGGCCTGCAG
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/db_xref="taxon:05606"
/db_xref="taxon:05606"
/dev_stage="Adult"
/dev_stage="Adult"
/ote="Organ: lung_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR-(U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ025993 449 bp DNA GSS 25-FEB-2000
RPCI-23-343116.TJ RPCI-23 Mus musculus genomic clone RPCI-23-343116
                                                                 Tel: +55-11-2704922

Fax: +55-11-2707001

Bmail: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QVO&t2=QVO-EN0102-081100-458-906&t3=2000-11-08&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 327.
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Zhao, S., Nlerman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  834 GCTCCTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCACCTTGGACACACTGCA 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           774 GGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATAGCGGCCTTTTCCTCTACCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 327;
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGGACGTCGCCGACTTTGCCACCACCATCTGGCAGCAGATG 936
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Unpublished (1999)
Other_GSSS: RPCI-23-343116.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.4%; Score 135.8; DB 1
89.6%; Pred. No. 1.8e-20;
tive 0; Mismatches 17
                                                                                                                                                                                                                                                                                                      1. .327
/organism="Homo sapiens"
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                                                Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                  1. .464
//organism="loss taurus"
//db_xref="taxon:9913"
//clone_lib="MARC_2BOV"
//lab_host="DH108"
//lab_host="DH108"
//note="Vector: pcMv SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
// a 152 c 128 g 87 t
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1 (bases 1 to 32).

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,Cs., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF848766 327 bp mRNA EST 16-JAN-2001
VOO-ENW102-081100-458-g06 EN0102 Homo sapiens CDNA, mRNA sequence.
BF848766 GI:12235903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \operatorname{Simpson}, A.\operatorname{J} Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CGACCCTTCTGCTGGAGGCAGTGACAGCGCGGGACAGCTGGGCCCCACTTCTCCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 CATCCTCTCTGCTGCACCTTTCTGGGCAGGTCCGCCTCCTTCTTGGGGCCCTGCAGGGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 GCTTGGGAGAATGGAAAACCCAGATGGAGGAGCACAAGGCACAGGACATTCTGGGAGCAG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 CATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTTCGGGGCCCTGCAGAGCC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383 TCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGGTTCACAAGGATCCCAATGCCA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443 TCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAG 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCTTGGGAGAATGGAAAACCCAGACGGAGCAGACCAAAGCACAGGACGTCCTGGGAACCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 TCTTCCTGAGCTTCCAACAGCTGCTCCGAGGAAAGGTGCGCTTCCTGCTGCTGTTGTAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 TGACCCTTCTGCTGGAGGGAGTGATGGCAGGGGGGACAAACTGGGACCCACTTGCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 464;
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20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 227.8; DB 10; Length
Pred. No. 5.1e-41;
0; Mismatches 27; Indels
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                                           BACKWARD: GTTTTCCCAGTCACGACG
Plate: 54 row: J column: 23
Seq primer: ATTTAGGTGACACTATAG.
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Laboratory of Cancer Genetics
                                                                                                                   Location/Qualifiers
                          FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.8%;
87.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 20.8
Best Local Similarity 87.2
Matches 266; Conservative
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PCR PRimers
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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
BcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
121 c 108 g 129 t lothers
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library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bcapec.med.buffalo.edu/corderingframe.htm) or from Resea of Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 343 row: I column: 16 Seq primer: Specific Security Secur
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A2352219 419 bp DNA GSS 29-SEP-2000
1M0090P05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0090P05 R, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 GCAGGTTCGCCTCCTCTTGGGGGCCCTGCAGGGCCTCCTAGGAACCCAGGTAAGTCCCCA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 ACAGGTCCGTCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-343116"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/lab_host="DH10B"
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                    1. .449
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δ g ò QQ δ g

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114)gblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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2M0046I05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0046I05 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PMP42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.7%; Score 106.2; DB 13; Length 419; 79.2%; Pred. No. 8.1e-14; Live 0; Mismatches 33; Indels 0;
                                                                                                                                                                                                                                                                                                                                         /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 GCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGT 518
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      Std Error: 0.00
Insert Length: 10000 Std Error: C
Plate: 0090 row: P column: 05
Seq primer: CACACGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 419.
                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0090P05"
                                                                                                                                                            Location/Qualifiers
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                                                                                     S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0046105"
/clone_lib="Mouse 10kb plasmid UUGClM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 86.4; DB 13; Length 708;
Pred. No. 2.5e-09;
0; Mismatches 41; Indels 0
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20:84112, USA
                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0046 row: I column: 05
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 708.
Location/Qualifiers
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
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Best Local Similarity 73.0°
Matches 111; Conservative
                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 589)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1;to 752) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. ar
                                                                                                                                                                                                                                                                                                               High Throughput Sequencing Center

Notersity of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Exa: (206) 616-38887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       509 GAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTAACGCTCAGCTGCT 568
                                                                                                                                                                          Sequence-tagged connectors: A sequence approach to mapping and
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                             scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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Plate: 3106 row: D column: 7
Seq primer: M13 Reverse
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Pred. No. 2.1e-07;
                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3106 Col=7 Row=D"
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Location/Qualifiers
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68.08;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Glibert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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Pteryyota; Neoptera; Endopteryyota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov g column: 06
High quality sequence stop: 587.
Location/Qualifiers
                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 65.6; DB 10; Length 589;
Pred. No. 0.00011;
0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3533885"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample="/dev_stage="3 months, virgin"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 rccagcccggcrccrccrgcrrgrgaccrccgagrccrcagraa 104
Contact: Robert Strausberg, Ph.D.
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AL053013
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Drosophila melanogaster
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KEYWORDS
SOURCE
ORGANISM
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JOURNAL
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Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for Mybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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ilarity 15.5%; Pred. No. 0.031;
Conservative 174; Mismatches 18
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="RACR19916"
/note="end : TET3"
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Matches 66; Conserv
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